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AC027717 Homo sapiens chr
AC010217 Homo sapiens chr
AC010272 Homo sapiens chr
AC011940 Homo sapiens clo
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1 (bases 1 to 1318)

2 and Schendel, D.J.

Tumor-infiltrating lymphocytes recognizing spontaneously arising rumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of a reconstry immune response
                                                                                                                                                                                                                                                J gene; junction; T cell receptor; TCR junctional sequence; V gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission Direct Submission Programmed (11-JUN-1996) P. Jantzer, Institute for Immunology, Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology, Goethestr. 31, D- 80336 Munich, PRG Goethestr. 31, D- 2011
                                                                                                                                                                         08-JAN-1997
                                                                                                                                                                                              H.saplens mRNA for rearranged TCR junctional sequences
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/codon_start=1
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08-881509-7 x HSTCRJUNC
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                                             gb_htg13:AC027717
gb_htg3:AC010217
gb_htg3:AC010272
gb_htg4:AC011940
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AC016554 Homo sapiens chromd
AC004999 Homo sapiens PAC cl
AL359961 Homo sapiens chromd
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-WODEL-frame+-Par.model-par.model-groundt_28032001_092236_29744/app_query.fasta_1.
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-MAXIEN-2000000000 -USER-DECLOUX-08-88159-THREADS=1
-NCPU=6 -ICPU=3 -LONGLOG -NO_XLPXY -WAIT -THREADS=1
                                                                                                                                                            About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database length: 1736092196
Search time (sec): 3669.890000
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Query: 08-881509-7
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9b_htg17:AC073896
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gb_htg22;AL359961
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gb_htg4:AC012346
gb_htg10:AC024315
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gb_ba2:PP2ABLIGG
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9b_htg8: AC021669
9b_pr3: AC009319
9b_htg14: AC048347
9b_htg3: AC010758
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gb_htg15:AC064575
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gb_htg8:AC021520
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LOCUS S69140 98 bp mRNA PRI 23-SEP-1994
DEFINITION TCR V alpha-T-cell receptor alpha-chain (allergen-specific) [human, grass.sensitive individual VI 19, Peripheral blood, mRNA Partial,
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Mohapatra, S.S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P.,
Mogil, E. and Romagnani, S.
Molecular basis of cross-reactivity among allergen-specific human T.
Immunology 81 (1), 15-20 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/note="This sequence comes from Fig. 3b; Protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 144562] from the original journal article.
Location/Qualifiers
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                                                                                                                                                                                                 /note="unnamed protein product"
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/note="T-cell receptor alpha-chain"
                                                                  Treells specific for kidney carcinome
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMH (DE)
Location/Qualifiers
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Б
               unidentified
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1 (bases 1 to 39)
Schendel, D.J.
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REMARK
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is in conflict with the conceptual translation.

/codon_start=1
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85.714 Percent Identity: 78.571
                                                                                                                                                                                                                                                                                                                               16 TTCTGTGCAGCCTTACCTGGTTCTGCAAGGCAACTGACCTTT 57
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Percent Identity: 78.571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T-cells specific for kidney carcinome
Patent: EP 0816496-A 07-JAN-1998:
BOEHRINGER MANNHEIM GMBH (DE)
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/db_xref="taxon:32644"
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A93127.1 GI:6741516
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Schendel, D. J.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens chromosome 18 clone RP11-129F9 map 18, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                           Cloud expansion of myelin basic protein-reactive T cells in patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence Eur. J. Immunol. 25 (4), 958-968 (1995)
                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata: Craniata: Vertebrata; Euteleostomi; Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 87) (Vandevyver, C., Mertens, N., van den Elsen, P., Medaer, R., Raus, J. and Vandevyver, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Partial TCRVA (1. .15), TCRNA (16. .18), TCRJA (19. .75), partial TCRCA (76. .87)" /codon_start=1
                                                                              LOCUS HUMTCRACG 87 bp mRNA PRI 07-NOV-1995
DEFINITION Homo saplens (clone NS1-F4) T cell receptor alpha chain (TCRA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"YFCAEASGSARQLTFGSGTQLTVLPDIQK"
19 c 21 g 27 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="GDB:G00-120-404"
/product-T_Cell receptor alpha chain"
/protein_id="AAA80964.1"
/db_xref="GI:853663"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 64.286
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                 172801.1 GI:853662
T cell receptor alpha.
Homo sapiens (Clone: NSI-F4) cDNA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="NS1-F4"
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Locus AC021669 1:
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2. [bases 1 to 157437)

Seckerly, R., Beda, F., Allen, N., Beckerly, R., Beda, F., Allen, N., Barderson, S., Baldwin, L., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, L., Barna, N., Beckerly, R., Beda, F., Boukhgalter, B., Brown, A., Burkett, G., Coste, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Galagan, J., Perrellano, K., Domino, M., Doyle, M., Fenestor, J., Garata, P., FitzHugh, M., Porrest, C., Galagan, J., Garata, P., Haeford, A., Horton, L., Landers, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, C., Liu, G., Locke, N., Landers, T., Lehoczky, J., Leyhe, R., Johnson, P., McCharl, L., Morrow, J., Naylor, J., Machan, D., McPheeters, R., Mardul, J., Meneus, L., Morrow, J., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, R., Suhce, R., Severy, P., Raymond, C., Riley, R., Rothman, D., Pizan, C., Subramanian, R., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., and Zody, M., Viel, R., Wol, X., Wyman, D., Ye, W.J., Charles, A., and Zody, M., Viel, R., Wol, X., Wyman, D., Ye, W.J., Charles, A., and Zody, M., Viel, R., Wol, X., Wyman, D., Ye, W.J., Charles, A., and Zody, M., Viel, R., Wol, X., Wyman, D., Ye, W.J., Charles, A., and Zody, M.
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://fpgenome.washington.edu/RM/RepeatMasker.html
http://fpgenome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research
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Center code: WISR
web site: http://www.seq.wi.mit.edu
web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Conter project name: L1300
Center project name: L29_F9
Center projec
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Insert size: 157437; sum-of-contigs
Quality coverage: 4.9 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
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39086: contig of 9673 bp in length
gap of unknown length
99008: contig of 9922 bp in length
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5817: contig of 2683 bp in length
gap of unknown length
10828: contig of 5011 bp in length
gap of unknown length
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21956: contig of 7052 bp in length
gap of unknown length
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gap of unknown length
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3134: contig of 1838 bp in length
1 (bases 1 to 157437)
Birren,B. Linton,L., Nusbaum,C. and Lander,E.
Birnen,B., Linton,L., Nusbaum,C. and Lander,E.
Grown sapiens chromosome 18, clone RP11-129F9
Unpublished
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gap of unknown length
74733: contig of 13479 bp in length
gap of unknown length
gap of unknown length
104301: contig of 15451 bp in length
gap of unknown length
contig of 15627 bp in length
gap of unknown length
contig of 15027 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-129F9"
/Clone_lib="RPCI-11 Human Male BAC"
39877 a 39144 c 38679 g 39736 t l Others
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches for a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse Sequences.

Genes and Region of Sequence similarity are identified by BLAST EST and CDNA Sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences identical matches are annotated as similar.
                       Worley, K.C.
Direct Submission
Submitted (16-AUG-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                               Submitted (28-UUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only the insert may be found in the record for the remainder of Overlapping clones are noted at the beginning and end of the Features listing.
                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (25-Aug-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor plaza, Houston, TX 77030, USA
ON 501 28, 2000 this sequence version replaced gi:9438826.
gc-help@bcm.tnc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEDUENCING READ COVERAGE: Sequencing is completed to a minimum retands with no ambiguities or 2 chemistries with a minimum of 2 clones and 2 clones and 3 reads with no ambiguities or 1 chemistries with a minimum of 2 a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              938. ..6929° ' '
/note="Unigene cluster similar to: SEG_HSLPP Human lipoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="(TATATG)n"
938. .6929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
(bases 1 to 172581)
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784. 825
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                                                                                                                                                                                    Worley, K.C.
Direct Submission
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                                           TITLE
JOURNAL
                       AUTHORS
                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                     JOURNAL,
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                                                                                                                                                                                                                                                                                                                                           AUTHORS
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// note="Region similar to: Hs#S1813459
UI-HF-BNO-alf-f-08-0-UI.rl Homo sapiens cDNA: AW503943"
Complement (16516. .17018)
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17132. .1732. .1733
/note="Region similar to: Hs#S2010443 EST387857 Homo sapiens cDNA: AW975748"
                                                                                                                                                                                                                                                                                                complement (13047. 13192)
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/rpt_family="MIR"
complement(13910. 14180)
/note="region similar to: Hs#S1034663 oml0hll.s1 Homo.ynote="region similar to: sapiens cDNA: AA907068"
complement(14381. 14842)
                                                                                                                                     /rpt_family="AT_rich".

complement(9379. 9851)

/note="Region similar to: Hs#S1816152 hd44d11.x1 Homo

/note="Region similar to: Hs#S1816152 hd44d11.x1 Homo

sapiens CDNA: AW511222"
preferred partner (LPP) gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(25074. .25376)
/rpt_family="AluSx"
25419. .25705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /rpt_family="L1ME"
complement(25706. .25981)
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/rpt_family="L2"
complement(21429, 21723)
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1804. .21912
rpt fr. .21912
                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="L1PA3"
4843.
                                                                                                                                                                                                                                                       _family="Alux"
. . .12620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="AT_rich"
24159. .24458
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                                                                                                /rpt_family="Alux"
1933. .9073
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt_family="AT_rich"
15606. .156~1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -"L1ME3A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AluSx"
23767. .23033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family-"AluSq"
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1990. .22716
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15195. .15216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pt_family="(CA)n"
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/rpt_family="L1"
                                                        /rpt_family="A-rich"
8121. .8205
              6449. .6622
/rpt_family="AluJo"
7630. .7677
                                                                                                                                                                                                                                                  /rpt_family="Alux" complement(11625...
                                                                                                   complement(8904.
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Mammalia; Eutneria; Filmudues, Cacathinia, Commendia; Eutneria; Filmudues, Cacathinia, Carlobases 1 to 178814)

Richard, Dan, Adams, C., Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Carter, M., Chacko, J., Chen, Z., Cox, Cox, Bonxie, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox, C., Ferraguto, D., David, R., Delgado, O., Deshaco, D., Ding, Y., Domah-Rashld, N., David, R., Delgado, O., Land, R. J., Ferrandez, C., Ferraguto, D., Forcum Transey, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, L., Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L. Li, Jia, Y., Jones, M., Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jones, M., Kelly, S., Kondelgewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, M., Logan, O., Lozado, R.J., Lu, J., Liu, J., Liu, M., Logan, C., McLeod, M.P., Mei, G., Morgan, M., Lucler, R., Martin, R., Martin, R., Martin, S., Payton, B., Perez, L., Villson, R., Sucgang, R., Shah, B., Parkon, S., Payton, B., Stamps, A., Taylor, T., Vasqiez, L., Villson, R., Vo, O., Wahbah, M., Tabor, P., Taylor, T., Vasqiez, L., Villson, R., Vo, O., Wahbah, M., Valle, P., Taylor, T., Waren, J., Wrenstork, G., Yu, W., Zhou, X., Nelson, D., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LOGUS #A048847 175814 bp DNA
LOGUS AAC48847 175816 bb. Braft
DEFINITION Home sapiens Chromosome 12 clone RP11-367612, WORKING DRAFT
SEQUENCE, 19 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 57.143
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                                                                                                                                                                                                                                                                                                                                              /rpt_family="Alusq"
32348 .32560
/rpt_family="Try" | 72560
/rpt_family="(Try)n"
complement(33728 .34028)
/rpt_family=".
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34159. .34213
                                                                                                                                                                                                                                                     /rpt_family="MER20"
31990. 320AA
                                                                                                        /rpt_family="Alusx"
28306. .28067
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                                                                                           /rpt_family="AT_rich" complement(26752. .27
/rpt_family="AluSc"
25982. 26255
/rpt_family="LiME"
26602. 26657
                                                                                                                                                                                      /rpt_family="MER67B"
31541. .31633
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complement(32041. .3
                                                                                                                                                                                                                                     'rpt_family="L1MA7"
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2 (bases 1 to 175814)
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Ratio: 4.083
Percent Similarity: 85.714
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08-881509-7 x AC009319
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AUTHORS JOURNAL

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* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                BASE COUNT
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                              Submitted (14-APR-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                         Chemistry: Dye-primar Bodipy: 28% of reads
Chemistry: Dye-terminator Big Dye: 72% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 155020 bases at least 040
Consensus quality: 15521 bases at least 020
Consensus quality: 17034 bases at least 020
Estimated insert size: 170493; sum-of-configs estimation
Quality coverage: 0x in 020 bases; sum-of-contigs estimation
Quality coverage: 3.6x in 020 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See http://www.hgsc.bcm.tmc.eduddosgGebbank.draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 19 contigs. The true order of the pieces arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: Estimated insert size may differ from sequence length
                                                                               On Aug 31, 2000 this sequence version replaced gi:9930656.
Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of unknown length
contig of 26949 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of unknown length
contig of 21001 bp in length
are of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29811: contig of 29811 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of 15080 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 11231 bp in length
gap of unknown length
contig of 10042 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10474 bp in length
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gap of unknown length
contig of 5244 bp in length
gap of unknown length
contig of 7453 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown length
of 3436 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 1734 bp in length.
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                                                                                                                                                  gap of unknown length
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of 5490 bp in l
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                                                                                                                                                                                                                                           Sequencing vector: M13; L08821
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               Direct Submission
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Worley, K.C.
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Birren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Balren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Brana, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Gooke, P., Castle, A., Colangelo, M., Collins, S., Collymore, A., Ferreira, P., Flethugh, W., Fowrest, C., Funke, R., Gage, D., Ferreira, P., Flethugh, W., Fowrest, C., Funke, R., Gage, D., Laddyn, S., Grant, G., Hagos, B., Haedrord, A., Horton, L., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McDaurk, A., McGurk, R., McLaughlin, J., Melorim, J., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thoman, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W. J., Zimmer, A. and Zody, M., Wheeler, J., Wu, X., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 258550)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (22-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Aug 31, 2000 this sequence version replaced 9i:9280749.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                            1828 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67881 TACTGCATTCCTATCGCTCTTCCAGGTCTCTCACATTC 67922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                  Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrCysLeuAlaLeuAlaGlySerAlaArgGlnLeuThrPhe 14
                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-367G12"
50954 a 35383 c 35133 g 52516 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AC048347 from: 1 to: 175814
                                                                                                                                                                                                                                                                                   Length:
Location/Qualifiers
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Homo sapiens, clone RP11-1B18
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85.714
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                                                                                                                                                                                                                                                                                                                 Percent Similarity:
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                   source
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consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as some as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1423: gap of 100 bp 100
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57160 c 56642 g 69733 t 3704 others
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190362: contig of 14121 bp in length
0462: gap of 100 bp
208674: contig of 18212 bp in length
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228999: contig of 20225 bp in length
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                                                                                                                                                                                                                                             184 2283; gap of 100 bp 2284 5870; contig of 3587 bp in length 2284 5870; contig of 3587 bp in length
                                                                                                                                                                                                                                                                                     2184 2283; gap of 100 bp 2284 5870; contig of 3587 bp in length 5871 5970; gap of 100 bp 5971 13493; contig of 7523 bp in length
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Percent Identity: 64.286
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/db_xref="taxon:9606"
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176141: cont.
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31323: cont
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08-881509-7 x AC010758
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Ratio:
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Chases 1 to 73806)

Rizren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N. Birren, B., Linton, L., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 73806)
                                                                                                                                                                                                                                                                 Submitted (15-OCT-1998) Cross S.M., Queensland Institute of Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG 13-JUL-2000 HTG 13-JUL-2000 HTG 13-JUL-2000 Sequence chromosome 17 clone RP11-329H16 map 17, LOW-PASS SEQUENCE SAMPLING.
                                                                                                                                                                                                                                                                                                                         Z (bases 1 to 42)
Misko, I.S., Cross, S.M., Khanna, R., Elliott, S.L., Schmidt, C.,
Misko, I.S., Cross, S.L.
Pye, S.J. and Slins, S.L.
Crossreactive recognition of viral, self, and bacterial peptide
Crossreactive recognition of viral, self, and bacterial peptide
Ligands by human class I-restricted cytotoxic T lymphocyte
Ligands by human class I-restricted cytotoxic T lymphocyte
clonotypes: implications for molecular mimicry in autoimmune
HSA235208 42 bp mRNA HOMO SAPIED 12-WAR-1999 HOMO SAPIENS MRNA for T cell receptor alpha chain V-J junctional region (TCRAV7AJ16S3).
                                                                                                                r cell receptor; T cell receptor alpha chain; variable region.
                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 42)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2279-2284 (1999) 99162595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homos appiens chromosome 17, clone RP11-329416 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cell_type="cytotoxic T lymphocyte"
/cell_line="SP1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606"
/haplotype="A1, A2, B8, B45, Bw6"
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AC021520.2 GI:9148483
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Percent Similarity: 92.308
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6
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Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Castle,A., Choepel, Y. Colangelo,M., Collins,S., Collymore,A., Cooke,P., Dewar,K., Domino,M., Doyle,M., Fenestor,J., FitzHugh,W., Forrest,C., Gage,D., Galagan,J., Howland,J.C., Johnson,B., Hadord,A., Horton,L., Landers,T., Lehocsky,J., Levins,E., Kann,L., Karatas,A., Klein,J., Mardons,R., Leu,C., Liu,G., Locke,K., McDheeters,R., Meldrin,J., Meneus,L., Morlw,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., Ollyar,T., Peterson, K., Roy,A., Santos,R., Severy,P., Spencer,B., Stange-Thoman,D., Tirrell,A., Vassiliev,H., Viel,R., Talamas,J., Tesfaye,S., Theodore,J., Zimmer,A., and Zody,M., Zimmer,A., and Zody,M., Zimmer,A., Wassiliev,H., Viel,R., Vo,A., Wuxan,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                  Submitted (16-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 326 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                * NOTE: This record contains 76 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* identifying clones that may be gene-rich and allows
* identifying relationships among clones to be deduced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
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895 bp in length
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Web site: http://www-seg.wi.mit.edu
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11607:
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7680: con
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8666: con
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12583: conf
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4760; co
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5725: coi
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6720: co
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9637: co
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8616: gap of 100 bp 1900.
19500: contig of 884 bp in length 20455: contig of 855 bp in length 10555: gap of 100 bp 21441: contig of 886 bp in length 1541: gap of 100 bp 100 bp 1541: contig of 877 bp in length 1541: gap of 100 bp 
15537 15636: gap of 100 bp
15637 16521: contig of 885 bp in length
16522 16621: gap of 100 bp
16622 17518: contig of 897 bp in length
                                                                                                                                         17519 17618; gap of 100 bp 17619 18516; contig of 898 bp in length
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rf 886 bp in length
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24342: contig of 866 bp in length
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30154: contig of 906 bp in length
30254: contig of 906 bp in length
100 pp
1124: contig of 870 bp in length
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1888 bp in length
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rf 870 bp in length
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: gap of
19500:
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19601 20455: con
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27194:
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29148: con+
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35771: cont
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43606: cont.
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39678: conf
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42631: cont
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50430: cont
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53697; cont
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16130: cont
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21414: cont
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33770: con'
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69382: con'
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72257: cont
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I (bases 1 to 114541)

Burton,J.

Direct Submission

Submitted (06-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CBIO 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 9, 2000 this sequence version replaced gi:9715666.
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LOGUS AL391001 114541 bp DNA HTG 06-SEP-2000
DEFINITION Homo sapiens chromosome 1 clone RP11-477H21, *** SEQUENCING IN
PROGRESS ***, 30 unordered pieces.
                                                                                          ap of 100 bp in length 
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f 899 bp in length
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68104: contig of 881 bp in length
68204: gap of 100 bp
69094: contig of 890 bp in length
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gap of 100 bp
59: contig of 902 bp in length
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55333: contig of
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65168: con+4
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60220: cont
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53385: con'
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61212: cont
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63167: con
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66137: cont
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 92902 bases at least Q40
Consensus quality: 99799 bases at least Q20
Consensus quality: 99799 bases at least Q20
Insert size: 11641; sum-of-contigs
Consent size: 11641; sum-of-contigs
Consert size: 172321; 12.8% error; agarose-fp
Quality coverage: 1.80x in Q20 bases; sum-of-contigs Quality
coverage: 2.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4833 4932: gap of 100 bp
4933 7653: contig of 2721 bp in length
7654 7753: gap of 100 bp
7754 10006: contig of 2253 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 2540: contig of 2540 bp in length
2541 2640: gap of 100 bp
2641 4832: contig of 2192 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21514: gap of 100 bp
23969: contig of 2455 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33870: gap of 100 bp
37774: contig of 3904 bp in length
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contig of 3182 bp in length
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58844: contig of 2596 bp in length
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contig of 8043 bp in length
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contig of 2775 bp in length
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81153 87059: contig of 5907 bp in length
87060 87159: gap of 100 bp
87160 94342: contig of 7183 bp in length
                 Contact: humquery@sanger.ac.uk
Web site: http://www.sanger.ac.uk
                                                                                                            ...-- Summary Statistics
                                                                                  Center project name: bA477H21
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104972 105071: gap of 100 bp
105072 112223: contig of 7152 bp in length
112224 112323: gap of 100 bp
112324 114541: contig of 2218 bp in length.
Location/Qualifiers
94343 94442: gap of 100 bp
9443 97259: contig of 2817 bp in length
97260 97359: gap of 100 bp
97360 99869: contig of 2510 bp in length
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Dipublished

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E (bases I to 159511)

S Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,

Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B.,

Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A.,

Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,

Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D.,

Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J.,

McTow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,

Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,

Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,

Wyman, D., Ye, W. J., Zimmer, A., and Zody, M.

Direct, Submission
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatWasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 159511)
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Locus AC012346 1
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Ratio:
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KEYWORDS
SOURCE
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/db_xref="taxon:9606"
/clone="RP11-15N22"
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49386. .54379
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                                      ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                            Center clone name: 15_N_22
Center clone name: 15_N_22
Center clone name: 15_N_22
Sequencing vector: M13; M77815; 100% of reads
Sequencing vector: M13; M77816; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 155739 bases at least Q30
Consensus quality: 154777 bases at least Q30
Consensus quality: 154777 bases at least Q30
Insert size: 168000; agarose-fp
Insert size: 168711; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; sum-of-contigs
Quality coverage: 3.9 in Q20 bases; sum-of-contigs
                                                                                                                   Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
...----- Project Information
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54379: contig of 4994 bp in length
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83893: contig of 9544 bp in length
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contig of 4512 bp in length
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23587: contig of 3064 bp in length
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15547: contig of 3286 bp in length
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contig of 1258 bp in length
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contig of 1612 bp in length
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45905; conti
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36870; cont
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60438: cont
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18501: cont
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9218: con
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1119 2144: co
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vector_side:right"
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Burkath B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Burker, B., Linton, J., Barna, N., Beda, F., Boguslavkiy, L., Chanderson, S., Baldwin, J., Barna, N., Beda, F., Boguslavkiy, L., Choppela, P., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choppela, Y., Colangelo, M., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Grandra, J., Gardyna, S., Ginde, S., Goyette, M., Graham, D., Grand-Pierre, N., Grant, G., Lilev, I., Johnson, R., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Looke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., Mocheeters, R., Maldrim, J., Morman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Ollyvar, T. M., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Ollyvar, T. M., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stange-Thomann, N., Stojanovic, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Yo, A., Wilson, J., Zimmer, A. and
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Homo sapiens clone RP11-26N3, WORKING DRAFT SEQUENCE, 14 unordered
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Birren,B., Linton,L., Nusbaum,C. and Lander,E.
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                               2801 others
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                                                                  128806. .142048
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142149. .159511
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a 29248 c 29765 g 47114 t
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AC024315.3 GI:8072573
HTG: HTGS_PHASE1; HTGS_DRAFT.
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08-881509-7 x AC012346
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LOCUS AC024315 1
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                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                    50583
                                                                                                                               misc_feature
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                                                                                                                                                                                 BASE COUNT
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VERSION

TITLE

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* NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                      Center Clone name: 26_K.3

Center Clone name: 26_K.3

Sequencing vector: M13 M77815. 100% of reads Chemistry: Dye-terminator Big bye: 100% of reads Assembly program: Phrap; version 0.960731

Consensus quality: 154942 bases at least 030

Consensus quality: 165969 bases at least 030

Consensus quality: 165505 bases at least 030

Consensus quality: 162505 bases at least 030

Insert size: 164000; agarose-fp

Insert size: 164558; sum-of-contigs

Quality coverage: 4.6 in 020 bases; sum-of-contigs
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11791 11890: gap of 100 bp 18654 18753: contig of 6763 bp in length 18654 18753: gap of 100 bp 18754 27335: contig of 6882 bp in length 27336 27435: gap of 100 bp 27436 41698: contig of 14263 bp in length
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54767: contig of 12969 bp in length
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88083 110113: contig of 22031 bp in length
110114 110213: gap of 100 bp
110214 133760: contig of 23547 bp in length
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133861 165858: contig of 31998 bp in length.
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4607 6447: contig of 1841 bp in length
6448 6547: gap of 100 bp
6548 11790: contig of 5243 bp in length
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/note="assembly_fragment"
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/note="assembly_fragment
                                                                                 Center project name: L4668
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4607 6447: cor
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GenBank staff at the National Library of Medicine created this entry lorg gibbs 68879] from the original journal article.
This sequence comes from Figure 4.
Location/Qualiflers
I. 716
/ Organism="Homo sapiens"
/ Ab_xref="taxon:9606"
I. 716
/ Apene="TCR V alpha"
/ Note="TCR V alpha"
/ Apene="TCR V alpha"
/ Apene="TLS V alpha"
/ A
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1 (Dases 1 to 716)
Griesinger,F., Jansen,B. and Kersey,J.H.

Differentiation in mature T lymphoid leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seg_documentation_block: 716 bp DNA PRI 04-MAY-2000 563879 563879 DEFINITION TCR V alpha "T cell receptor variable alpha chain [human, MT-ALL, Genomic Mutant, 716 nt].
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Percent Identity: 90.909
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J. Immunol. 147 (10), 3336-3341 (1991)
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/note="assembly_fragment"
133861. 165858
/note="assembly_fragment"
a 34483 c 34023 g 47184 t
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                                                                                                                                   77436. .41698
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54868. .70875
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18754. .27335
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S63879.1 GI:238692
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4.800
90.909
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Ratio:
Percent Similarity:
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SSRALYSVHWYROKHGEAPVFLMILLKGGEOKGHEKISASFNEKKOOSSLYLTASGLS
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SSRALYSVHWYROKHGEAPVFLMILLKGGEOKGHEKISASFNIK
A150 a 159 c 177 g 183 t

Caps: 0

Ratio: 3.97

Caps: 0

A150 c 177 g 183 t

Caps: 0

Caps: 0
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o sapiens chr
o sapiens chr
o sapiens chr
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LVLSGSARQLTFGXCLVGGSARQLTFGXCLVGGSARQLTFGXCLVGGSARQLTFGXCL
LVSGSARQLTFGXCLDSGSARQLTFGXCLVLSGSARQLTFGXCLVLSGSARQLTFGXCLV
LVSGSARQLTFGXCLVGGDTDKLIFGXCLVLSGSARQLTFGXCLVLSGSARQLTFGXCLV
VSGSARQLTFGXCLAGGSARQLTFGXCLALAGSARQLTFGXCLVBSGSARQLTFGXCL
VAGGGNTPLVFGXCLVGGSARQLTFGXCLVGSSARQLTFGXCLVGRSARQLTFGXCL
LVAGGGNTPLVFGXCLVGGSARQLTFGXCLVGSSARQLTFGXCL
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CLVVLGGSGGONLFGXCLVGRARAPGGATNKLIFGX
ATGSARQLTFGXCLVGRARAGNMLTFGXCLVATNQGRNCSDLW"
                                                                                                                                                                                                  J gene; junction; T cell receptor; TCR junctional sequence; V gene. human.
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                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Butheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 1318)
3 antzer, P.U. and Schendel, D.J.
Tumor-infiltrating lymphocytes recognizing spontaneously arising rumor-infiltrating lymphocytes recognizing catalogue.
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 i AC027717 HOMO & i AC010217 HOMO & i AC010272 HOMO & i AC011940 HOMO & i
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Submitted (11-JON-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
                                                                                                                                           08-JAN-1997
                                                                                                                                                       H.sapiens mRNA for rearranged TCR junctional sequences. X98410
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         151974
154690
155306
169075
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/note="V gene/J gene junction"
/codon_start=1
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           5.0e+03
5.1e+03
5.1e+03
5.5e+03
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A93131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
                                                                                                                                                   mRNA
              93.05
92.93
92.90
92.30
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                44.00
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LOCUS A93131
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08-881509-8 x HSTCRJUNC
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                                                                                                    seq_name: gb_pr7:HSTCRJUNC
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LOCUS HSTCRJUNC
                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                    gb_htg13:AC027717
gb_htg3:AC010217
gb_htg3:AC010272
gb_htg4:AC011940
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                                                                                                                                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       re Len | Documentation | ... RNA for rear | 1318 | 1x99410 | H.saplans mRNA for rear | 1318 | 1x99410 | H.saplans mcNa for rear | 134 | 1x99410 | Tex V alpha="r-cell recept | 134 | 1x99110 | Sequence | from Patent | 134 | 1x9910 | Homo saplans (Clone NSI-NS) | 157437 | AC01669 | Homo saplans chrome | 172814 | AC0048347 | Homo saplans chrome | 172814 | AC0048347 | Homo saplans chrome | 128856 | AC010758 | Homo saplans clone | 258550 | AC010758 | Homo saplans clone | 128856 | AC010758 | 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1887 | X63668 Pseudomonas plasmid DNA 8280 | X66604 Pseudomonas sp. plasmid 35112 | Ac001649 Drosophila melanogas 69017 | AL031732 Human DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  i ACO13749 Drosophila melanogas
i ACO13806 Mus musculus clone
i ACO16554 Homo sapiens chrome
i ACO04999 Homo sapiens PAC Cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL359961 Homo sapiens chromd
                                                                                                                                                          About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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112958
129541
148102
                                     OM of: 08-881509-8 to: GenEmbl:* out_format : pfs
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4.3e+03
4.9e+03
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197.00
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94.60
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194.90
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144.84
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108.72
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44.00
44.00
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Database sequences: 1118133
Database length: -1736092196
Search time (sec): 3669.890000
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Query: 08-881509-8
                                                                              Date: Apr 1, 2001 4:45 AM
                                                                                                                                                                  Command line parameters:
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9b_htg14:AC055413
9b_htg13:AC036305
9b_htg15:AC064575
9b_htg14:AC064575
9b_pr7:HUAC002299
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gb_htg6:AC016554
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gb_htg22:AL359961
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gb_htg14:AC048347
gb_htg3:AC010758
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gb_pr7:HSU30428
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gb_htg7:AC019749
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gb_ba2:PP2ABLIGG
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gb_htg4:AC012346
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gb_htg8:AC021669
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gb_htg8:AC021520
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gb_pr7:HSU40776
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gb_pat1:A93131
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KEYWORDS

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//Translation="MROYARVIVFLTLSTLSLAKTTQPISMDSYEGQEVNITCSHNNI
ATNDYITWYQQPPSQGPRFIIQGYKTKYTNEVASLFTPADRKSSTLSLPRVSLSDTAV
YYCLVGGSARQLTFGSGTQLTVLPDIONPDPAVYQLRDSKSSDKSVCLFTDFDSQTNV
SQSKDSDVYITDKTYLDMRSMDFKSNSAVAMSNKSDFACANAFNNSIIPEDTFFFPSPF
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// Ab_xref="G1:545974"
// translation="DSATYFCAALPESARQLTFGSGTQLTVLPDIQN"
            conflict with the conceptual translation"
                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                    1 TyrCysLeuAlaLeuAlaGlySerAlaArgGlnLeuThrPhe 14
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                                                                                                                                                       28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T-cells specific for kidney carcinome
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                           Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB69529.1"
/db_xref="GI:6741517"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: 'S69140 from: 1 to: 98
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1. .54
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Schendel, D.J.
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unclassified.
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08-881509-8 x S69140
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Mohapatra,S.S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P.,
Maggi,E. and Romagnani,S.
Molecular basis of cross-reactivity among allergen-specific human T
Immunology 81 (1), 15-20 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS
LOCUS
S69140
DEFINITION TCR V alpha=r-cell receptor alpha-chain (allergen-specific) [humar grass:sensitive individual VI 19, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="Tck v alpha"
/note="This sequence comes from Fig. 3b; Protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenBank staff at the National Library of Medicine created this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry [NCBI gibbsq 144562] from the original journal article.
This sequence comes from Fig. 3a.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="T-cell receptor alpha-chain"
                                                                                                                                                                                                                         /note="unnamed protein product"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                           /translation="CLVLSGSARQLTF"
                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                            /protein_id="CAB69531.1"
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                                                                                                                                                                      /organism="unidentified"
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/db_xref="taxon:9606"
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                                                                                                                                        Location/Qualifiers
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                                                 1 (bases 1 to 39)
Schendel, D.J.
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Percent Similarity: 100.000
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22-JAN-2000

DEFINITION

ACCESSION

ORGANISM

KEYWORDS

VERSION SOURCE REFERENCE AUTHORS

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RS Birren, B., Linchan, B., Birren, B., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Anderson, S., Baldwin, J., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Boquslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Cooke, P., Dekarlano, K., Donagelo, M., Collins, S., Collymore, A., Cooke, P., Ferreira, P., FitzHugh, W., Forrest, C., Gagae, D., Galagan, J., Ferreira, P., FitzHugh, W., Forrest, C., Gagae, D., Galagan, J., Howland, S., Craht, G., Hagos, B., Heaford, A., Horton, L., Howland, S., Craht, S., Levine, R., Liell, C., Liu, G., Locke, K., Maddand, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McRheeters, R., Meldrim, J., Morneal, C., Ramond, C., Riloy, R., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Pisani, C., Pollara, V., Raymond, C., Riloy, R., Theodore, J., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Zimmer, A. and Zody, M.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-Jan-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasKer:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Content: mt.pt./.www.seq.w..mit.cou

Content: sequence_submissions@genome.wi.mit.edu

Center project Information

Center clone name: 11300

Center clone name: 129_F_9

Sequencing vector: M13 m77815; 100% of reads

Chemistry: Dye-terminator Big Dye: 100% of reads

Assembly program: Phrap: version 0.960731

Assembly program: Phrap: version 0.960731

Consensus quality: 157720 bases at least 030

Consensus quality: 157720 bases at least 020

Consensus quality: 157720 bases at least 020

Insert size: 157437; sum-of-contigs

Quality coverage: 4.9 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1296: contig of 1296 bp in length
gap of unknown length
3134: contig of 1838 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
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1 (bases 1 to 157437)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 18, clone RP11-129F9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: WIBR
Web site: http://www-seg.wi.mit.edu
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gap of unknown
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of 7457
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gap of unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 5011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig of 4076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
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                                                                                                 (bases 1 to 157437)
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                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                       JOURNAL
                     REFERENCE
                                         AUTHORS
                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clonal expansion of myelin basic protein-reactive T cells in patients with multiple sclerosis: restricted T cell receptor V generangements and CDR3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                              Vandevyver,C., Mertens,N., van den Elsen,P., Medaer,R., Raus,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG 19-JAN-2000 HTG 19-JAN-2000 HOM Sapiens chromosome 18 clone RP11-129F9 map 18, WORKING DRAFT SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (19. .75), partial TCRCA (76. .87)"
/codon_start=1.475, 725, 220-120-404"
                                                                                                                                                                          Homo sapiens (clone NSI-F4) T cell receptor alpha chain (TCRA) IA2801
                                                                                                                                                             07 - NOV - 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="T cell receptor alpha chain"
/protein_id="AAA80964.1"
/db_xref="G1:853663"
/translation="FrcAEASGSARQLTFGSGTQLTVLPDIQK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 TTTTGTGCAGAGGCCTCTGGTTCTGCAAGGCAACTGACCTTT 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TyrCysLeuAlaLeuAlaGlySerAlaArgGlnLeuThrPhe 14
                             T cell receptor alpha.
Homo sapiens (clone: NS1-F4) cDNA to mRNA.
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [mmunol. 25 (4), 958-968 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="NS1-F4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /map="14q11.2"
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Locus AC021669 157437 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="TCRA"
                                                                                                                                                                                                                                                                 L42801.1 GI:853662
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                                                                                                   seq_name: gb_pr8:HUMTCRACG
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                                                                                                                                                 seq_documentation_block:
LOCUS
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Ratio:
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alignment_block:

BASE COUNT

gene

CDS

JOURNAL MEDLINE

TITLE

FEATURES

DEFINITION

ACCESSION KEYWORDS

VERSION

ORGANISM

SOURCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (Massa; 1 to 172581)

Muzny, D.M., Adams, C. Bailey, M., Barbaria, J., Blankenburg, K., Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C., David, R., Delgado, O., Deshazo, D., Ding, T., Domah-Rashid, N., Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D., Fordun-Tansey, J., Fernandez, C., Ferraguto, D., Gorrell, L.L., Guevara, W., Harris, K., He, X., Hernandez, J., Jackson, L., Lial, Y., Juncier, R., Martinez, C., McLeod, M. P., Kovar, C., Leal, B., Li, Z., Lichtarge, O., Liu, J., Liu, M., Logan, O., Mel, G., Moore, S., Moorish, T., Morgan, M., Mortis, S., Nash, S., Nash, S., Nashon, A., Nguyen, R., Nguyen, M., Nguyen, M., Nguyen, R., Nguyen, R., Nguyen, S., Osay, J., Scherer, S., Shah, E., Shen, H., Vasquez, L., Vinson, R., Voy, Wahbah, M., Wallington, S., Weinstock, T., When, J., Taylor, T., Wenstord, G., Yu, W., Tolan, M., Wallington, S., Weinstock, T. R., Williamson, A., Worley, K., Wren, J., When, J., Wellson, R., Vo, Wahbah, M., Wallington, S., Wenn, J., Werens, J., When, J., Wellson, R., Woll, Walliamson, A., Worley, K., Wren, J., When, J., Nelson, D., Taylor, J., When, J., Well, M., Nelson, S., Suppan, S., Osay, J., Taylor, T., Werensford, G., Yu, W., Naylor, S., Callang, K., Wenn, J., Weren, J., Werensford, G., Yu, W., Naylor, S., Callang, K., Wenn, J., Well, M., Wells, J., Well, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC009319 172581 bp DNA PRI 11-0CT-2000
Homo sapiens 3 BAC RP11-297K7 (Roswell Park Cancer Institute Human
AC009319
                                                                                           74733: Contig of 12246 bp in length gap of unknown length 89274: Contig of 14541 bp in length 104301: Contig of 15027 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 others
gap of unknown length
62487: contig of 13479 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                     contig of 18736 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                        contig of 34400 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AC021669 from: 1 to: 157437
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39877 a 39144 c 38679 g 39736 t 1 c
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Percent Identity: 64.286
                                                                                                                                                                                                                                                                     gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="18"
                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="RP11-129F9"
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                                                                                                                                                                                                                                                                                                        123037;
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Percent Similarity: 85.714
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08-881509-8 x AC021669/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sed_name: gb_pr3:AC009319
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LOCUS AC009319 17
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones overlapping clones are noted at the beginning and end of the
                                                                                        Submitted (16-AŭG-1999) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 172581)
                                                                                                                                                                                                                                                                      Submitted (28-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 172581)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-ANG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (25-AUG-2000) Human Genome Sequencing Center, Department
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA / On Jul 28, 2000 this sequence version replaced gi:9438826.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QUALITY OF INDIVIDUAL BASES This sequence meets stringent quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCING READ COVERAGE: Sequencing is completed to a minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            annotation as Low Coverage.
      (bases 1 to 172581)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 172581)
2 (bases 1 to 172 Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                         TITLE
                                                       TITLE
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/rpt_family="MIR"
complement(13910. .14180)
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complement(19962. .20058)
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complement(21429. .21723)
partner (LPP) gene"
                                                                                                                                                                                                                                                                                                             /rpt_family="AluY"
12336. .12639
'rpt f...
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complement(25706. .25981)
                                                                                8121. .8205
/rpt_family="CT-rich"
complement(8904. .9214)
/rpt_family="Alux"
                                                                                                                                                           8933. .9073
/function="Low Coverage"
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//rpt_family="AT_rich"
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preferred partner (LPP
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/rpt_family="AluJo"
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/rpt_family="A-rich"
                                                                                                                                                                                           1356. .9376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="AluSq"
24495, 24865
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                                                                                                                                                                                                                                                                                                    /rpt_family="AluY"
complement(11625.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 175814)

Sandota; B., Bauck, A., Barbaria, J., Blankenburg, K.,
Bodota; B., Bouck, J., Barooks, A., Bunab, C., Bunac, C.,
Burkett, C., Burrows, J., Carter, M., Chacko, J., Chen, Z., Cox.C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Duyan-Roccha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,
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Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLeod, M.P., Mei, G., Morgan, M.,
Morris, S., Nash, R., Say, J., Scherer, S.,
Guiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,
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Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC048347 175814 bp DNA HTG 01-SEP-2000 Homo sapiens chromosome 12 clone RP11-367G12, WORKING DRAFT SEQUENCE, 19 unordered pleces.
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85.714 Percent Identity: 57.143
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                                                                                                                                                                                                                     1541. 31633
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complement(31734. 31945)
/rpt_family"MER20"
31990. 32040
/rpt_family"(TA)n"
complement(32041. 32347)
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65082. 26657
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complement(26752. 2703
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HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="(TA)n"
complement(33728. .3
                                                                                                                                                                                                rpt_family-"MER67B"
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LOCUS AC048347 175814 bp
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Direct Submission
Unpublished
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08-881509-8 x AC009319
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JOURNAL

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* NOTE: This is a 'working draft' sequence. It currently
                          source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html). ONTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                    Sequencing vector: M13; L08821
Sequencing vector: M13; L08821
Sequencing vector: M13; L08821
Chemistry: Dye-primer Bodipy: 28 of reads
Chemistry: Dye-terminator B14 Dye: 72% of reads
Assembly program: Phrap; version 0.99329
Consenus quality: 156908 bases at least 040
Consensus quality: 170374 bases at least 020
Consensus quality: 170374 bases at least 020
Estimated insert size: 170493; sum-of-contigs estimation
Quality coverage: 0x in 020 bases; sum-of-contigs estimation
Quality coverage: 3.6x in 020 bases; sum-of-contigs estimation
           Direct Submission
Submitted (14-APR-2000) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                      contig of 15195 bp in length
gap of unknown length
contig of 15080 bp in length
gap of unknown length
contig of 10474 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 26949 bp in length
gap of unknown length
contig of 21001 bp in length
gap of unknown length
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29911: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 11231 bp in length
gap of unknown length
contig of 10042 bp in length
gap of unknown length
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gap of unknown length
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                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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gap of unknown
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gap of unknown
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gap of unknown
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Center project name: HATW
Center clone name: RP11-367612
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AUTHORS
TITLE
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RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baltren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boqualavkiy, L., Bouwingalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Castle, A., Castle, M., Colangelo, M., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FilzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., McEwan, P., McGurk, A., McKernan, R., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Kiley, R., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Direct Submission N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Direct Submission Street, Cambridge, MA 02141, USA on Aug 31, 2000 this sequence version replaced gi:9280749.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 258550)
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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                             1828 others
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Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 57.143
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                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/chcmosome="12"
/clone="RP11-367612"
50954 a 35383 c 35133 g 52516 t
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Location/Qualifiers
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AC010758
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Percent Similarity: 85.714
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consists of 20 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2184 2283: gap of 100 bp 2284 5870: contig of 3187 bp in length 5870: gap of 100 bp 10
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229100 258550: contig of 29451 bp in length.
Location/Qualifiers
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190463 208674: contig of 18212 bp in length
208675 208774: gap of
208775 228999: contig of 20225 bp in length
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/clone_lib="RPCI-11 Human Male BAC"
71311 a 57160 c 56642 g 69733 t 3704 c
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31423: gap of
38738: cont
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51477: cont
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67050: cont
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Align seg 1/1 to: AC010758 from: 1 to: 258550

1 TyrCysLeualaLeualaGlySeralaargGlnLeuThrPhe 14 :::||||||| 145471 TrcTGCCTTCGCGGGGGGGGGGGGGGGAATGACATTT 145512

seq_name: gb_pr6:HSA235208

seq_documentation_block:

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Submitted (15-OCT-1998) Cross S.M., Queensland Institute of Medical Research, The Bancroft Centre, 300 Herston Road, Brisbane, AUSTRALIA 4029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 73806)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Beckerly,R., Beda,F.,
HSA235208 42 bp mRNA PRI 12-MAR-1999
Homo sapiens mRNA for T cell receptor alpha chain V-J junctional
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-329H16
                                                                                                                                                                                                                                                                                                                                                                                                Crossreactive recognition of viral, self, and bacterial peptide ligands by human class I restricted cytotoxic T lymphocyte clonotypes: implications for molecular mimicry in autoimmune
                                                                                                    T cell receptor; T cell receptor alpha chain; variable region.
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 42)

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                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 42)
Misko,I.S., Gross,S.M., Khanna,R., Elliott,S.L., Schmidt,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2279-2284 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rearranged
/tissue_type="blood"
/cell_type="cytotoxic T lymphocyte"
/cell_line="SP1"
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/db_xref="taxon:9606"
/haplotype="A1, A2, B8, B45, Bw6"
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                                          (TCRAV7AJ16S3).
                                                                                AJ235208.1 GI:3851223
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LOCUS AC021520 73806 bp
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                                                                                                                                                 Homo sapiens
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48578: gap of
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Boguslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Domino, M., Doyle, M., Galagan, J., Gardt, G., Hagos, B., Hedford, A., Horton, L., Gardqan, S., Grant, G., Hagos, B., Hedford, A., Horton, L., Landers, T., Lehoczky, J., Levine, R., Jones, C., Kann, L., Karatas, A., Klein, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Norman, C. H., O'Connor, T. O'Donnell, P., Olivar, T. M., Peterson, K., Severy, P., Spencer, B., Stange-Thoman, D., Stojanovic, N., Subramanian, A., Talamas, J., Tasfaye, S., Theodore, J., Tirrell, A., Vassiliew, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Tirrell, A., Vassiliew, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Dimett, Street, Cambridge, Ma Oll, U. Sabantted (16-3Nn-2000) Whitehead Institute/MIT Center for Genome Submitted (16-3Nn-2000) Whitehead using RepeatMasker:

All repeats were identified using RepeatMasker:

Smit, A.F. A. & Green, P. (1996-11997)

Center: Whitehead Institute/ MIT Center for Genome Center Cenome Center Cenome Center Cenome Center Cenome Center Cenome Center Conterner Conterner Conterner Conterner Conterner Conterner Center Cenome Center Ce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: sequence_submissions@genome.wi.mit.edu ------ project Information Center project name: L5499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12683: gap of 100 bp
13570: contig of 887 bp in length
13670: gap of 100 bp
14560: contig of 890 bp in length
14660: gap of 100 bp
15536: contig of 876 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  863 962: contig of 862 bp in length
863 962: gap of 100 bp
963 1850: contig of 888 bp in length
1851 1950: gap of 100 bp
1951 2817: contig of 867 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p of 100 bp contig of 893 bp in length
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2918 3788: contig of 871 bp in length
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4760: contig of 872 bp in length
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contig of 895 bp in length
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f 886 bp in length
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contig of 871 bp in length
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f 860 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www-seq.wi.mit.edu
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8666: cor
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9637: cor
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6720: cor
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5725: co
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7680: co
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5726
5826
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2 42731: gap of 100 bp 107 45306: contig of 875 bp in length 107 43706: gap of 100 bp 100 bp 107 44539: gap of 100 bp 100 bp 107 4554: contig of 885 bp in length 107 4554: gap of 100 bp 107 45512: contig of 888 bp in length 107 45512: contig of 888 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                  19901 2003.5: Contray of 2005.5: gap of 20556 2055; gap of 20556 2041.2: contray of 886 bp in length 20556 2041.3: gap of 100 bp 2241.3: contray of 877 bp in length 2241.3: 2241.3: contray of 878 bp in length 23477 2476: gap of 100 bp 2477 24342: contray of 866 bp in length 23477 24342: contray of 866 bp in length 23473 24342: contray of 791 bp in length 25534 25333: gap of 100 bp 25534 25333: gap of 200 bp in length 25534 25333: gap of 200 bp in length 25534 25333: gap of 200 bp in length 25534 25532: contray of 860 bp in length 25534 25534 2500 bp in length 25534 256223: contray of 800 bp in length 25534 25623: contray of 800 bp in length 25534 26523: contray of 800 bp in length 255
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40673: contig of 895 bp in length
773: gap of 100 bp
41671: contig of 898 bp in length
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42631: contig of 860 bp in length
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39678: contig of 873 bp in length
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29249 30154: contig of 906 bp in length
30155 30254: gap of 100 bp
30255 31124: contig of 870 bp in length
31125 31224: gap of 100 bp
31225 32105: contig of 881 bp in length
32065: gap of 100 bp
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34927 35771: contig of 845 bp in length
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35872 36751; contig of 880 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 864 bp in length
15537 15636: gap of 100 bp

15637 16521: contig of 885 bp in length

16622 16621: gap of 100 bp

16622 17518: contig of 897 bp in length

17519 17618: gap of 100 bp

17619 18516: contig of 898 bp in length

1817 18616: gap of 100 bp

18617 19500: contig of 884 bp in length
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871 bp in length
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27194: contig of
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Page 9

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 114541)
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Burton,J.

Direct Submission

Submitted (06-SEP-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, Wr. E-mal.1 enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

On Sep 9, 2000 this sequence version replaced gi:9715666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo salens chromosome 1 clone RP11-477H21, *** SEQUENCING IN PROGRESS ***, 30 unordered pleces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 59354; gap of 100 bp 16.20: contig of 866 bp in length 16.12: contig of 895 bp in length 18.13: gap of 100 bp 18.13: gap of 100 bp 19.2555; gap of 100 bp 19.
             51431 51530; gap of 100 bp 52409; contig of 879 bp in length 52410 52509; gap of 100 bp
                                                                             09: gap of 100 pp
53385: contig of 876 bp in length
51430: contig of 900 bp in length
                                                                                                                                                                                      contig of 891 bp in length
                                                                                                                                                                                                                    ap of 100 bp contig of 857 bp in length
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                                                                                                                                                                                                                                                                                                                                                 contig of 893 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104: gap of 100 bp 69094: contig of 890 bp in length
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                                                                                                                                                                                                                                                                                                                      con.
                                                                                                                                                                                                                                                            con: gap of 56289;
                                                                                                                                                    85: gap of 54376: cont
                                                                                                                                                                                                                54476: gap of
55333: cont
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60220: cont
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66137: cont
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HTG: HTGS_PHASE1.
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08-881509-8 x AC021520
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Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 92902 bases at least Q40
Consensus quality: 97799 bases at least Q30
Consensus quality: 104556 bases at least Q30
Insert size: 111641; sum-of-contigs
Insert size: 11213; 12.8% error; agarose-fp
Quality coverage: 1.80x in Q20 bases; sum-of-contigs Quality
coverage: 2.06x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2540: contig of 2540 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7654 7753: gap of 100 bp 7754 10006: contig of 2253 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 100 bp contig of 2192 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of 100 bp contig of 2721 bp in length
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10107 16130: contig of 6024 bp in length
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contig of 5184 bp in length
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23969: contig of 2455 bp in length
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27263: contig of 3194 bp in length
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contig of 6407 bp in length
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72257: contig of 2775 bp in length
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                                                   Contact: humquery@sanger.ac.uk
                              Web site: http://www.sanger.ac.uk
                                                                                                                  Summary Statistics
                                                                                            Center project name: bA477H21
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44387:
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(4: gap of
66987:
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46994:
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102726 102825: gap of 100 bp 102826 104971: contig of 2146 bp in length 104972 105071: gap of 100 bp 105072 112223: contig of 7152 bp in length 112224 112323: gap of 100 bp 112324 114541: contig of 2218 bp in length. Location/Qualifiers
94343 94442: gap of 100 bp
94443 97259: contig of 2817 bp in length
97260 97359: gap of 100 bp
97360 97369: contig of 2510 bp in length
                                                                            99870 99969: gap of 100 bp 102225 contig of 2756 bp in length
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RS Birren, B., Linchon, L., Buckerly, R., Boquslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Baldwin, J., Barna, N., Beckerly, R., Boquslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Groke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galgagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Galgagan, J., Cardyna, R., Jones, C., Kann, L., Karatas, A., Klein, J., Howland, J.C., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, F., McGurk, A., McMaran, K., McLaughlin, J., Meldrim, J., McGwan, P., McJurk, A., Wriey, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Pirch, E., Mar, A., Lieu, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC012346 159511 bp DNA HTG 22-JUL-2000
HOMO sapiens clone RP11-15N22, WORKING DRAFT SEQUENCE, 29 unordered
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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l (bases 1 to 159511)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome, clone RP11-15N22
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31791 a 24051 c 23374 g 32420 t 23
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Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                     Center project name: 13497

Center clone name: 15_N_22

Center clone name: 15_N_22

Center clone name: 15_N_22

Sequencing vector: M13; M77815; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 145613 bases at least Q40

Consensus quality: 152390 bases at least Q30

Insert size: 168000; agarose-fp

Insert size: 156711; sum-of-contigs
Quality coverage: 3.6 in Q20 bases; agarose-fp

Quality coverage: 3.6 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                      NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pleces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1018: contig of 1018 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig of 1258 bp in length contig of 1612 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1019 1118: gap of 100 bp
1119 2144: contig of 1026 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61: gap of 100 bp
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47: gap of 100 bp
18501: contig of 2854 bp in length
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9319 12161: contig of 2843 bp in length
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32258: contig of 3181 bp in length
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83893: contig of 9544 bp in length
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54480 60438: contig of 5959 bp in length
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67094 74249: contig of 7156 bp in length
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                                                                                             ----- Project Information
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49285: con+
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9218: cor
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116071 116170: gap of 100 bp 116171 128705; contig of 12535 bp in length 128706 128805; gap of 100 bp 142048: contig of 13243 bp in length 142049 142148: gap of 100 bp
993: gap of 100 bp
92494: contig of 8501 bp in length
554: gap of 100 bp
102847: contig of 10253 bp in length
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ORIGIN

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Lupublished

Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birran, B., Linton, L., Nusbaum, C., Lander, E., Adouslavkly, L., Anderson, S., Baldwin, J., Barnaa, N., Beda, F., Boguslavkly, L., Colangalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Perreira, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Galagan, J., Grant, G., Hagos, B., Healford, A., Horton, L., Klein, J., Landers, T., Largos, B., Healford, M., Horton, L., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Klein, J., Landers, T., Largocque, K., Lehoczky, J., Levine, R., Lieu, C., Ille, T., Landers, M., Mcdennal, E., Marchan, P., Marginis, N., McCarthy, M., McBarn, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Mennan, C. H., O'Connor, T., O'Donnell, P., O'Nell, D., O'Connor, T., O'Donnell, P., O'Ivar, T. M., Spencer, B., Stange-Thomann, N., Stolano, S., Severy, P., Spencer, B., Stange-Thomann, N., Stolano, J., Tirrell, A., Travers, M., Trigillio, J., Yesman, T., Yeung, G., Zainoun, J., Zimmer, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC024\overline{3}15 165858 bp DNA HTG 26-MAY-2000 HOMO sapiens clone RP11-26N3, WORKING DRAFT SEQUENCE, 14 unordered
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All repeats were identified using RepeatMasKer:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.was.hington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 165858)
Birran, Bu. Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, Conne RP11-26N3
Unpublished
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Percent Identity: 64.286
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Percent Similarity: 85.714
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AUTHORS
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ACCESSION

KEYWORDS

VERSION SOURCE

AUTHORS REFERENCE

JOURNAL

TITLE

COMMENT

TITLE

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NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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Center clone name: 26_N_3

Sequencing vector: M13; M77812, 100% of reads

Sequencing vector: M13; M77812,

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 154942 bases at least Q40

Consensus quality: 162505 bases at least Q20

Consensus quality: 162505 bases at least Q20

Insert size: 164000; agarose-fp

Insert size: 164508; sum-of-cortigs

Quality coverage: 4.6 in Q20 bases; sum-of-contigs
                                 Contact: sequence_submissions@genome.wi.mit.edu
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110214 133760: contig of 23547 bp in length
133761 133860: gap of 100 bp
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Location/Qualifiers
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Web site: http://www-seq.wi.mit.edu
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/note="assembly_fragment
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/note="assembly_fragment
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/db_xref="taxon:9606"
                                                                                                                      Center project name: L4668
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133861 165858: conti
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18653: con
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1375 2528: con
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Eukaryota; Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.

[ tbases 1 to 716]
Griesinger, F., Jansen, B. and Kersey, J.H.

Differentiation in mature T lymphoid leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS S63879 716 bp DNA PRI 04-MAY-2000
DEFINITION TCR V alpha -T cell receptor variable alpha chain [human, MT-ALL,
Genomic Mutant, 716 nt].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 63879] from the original journal article. This sequence comes from Figure 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="T cell receptor variable alpha chain"
                                                                                                                                                                                                                                                                                                                                                                                                              misc_feature //note="assembly_fragment" //note="
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Percent Similarity: 90.909 Percent Identity: 90.909
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                                                                                                                                                                                      /note="assembly_fragment"
41799 .54767
/note="assembly_fragment"
54868 .70875
/note="assembly_fragment"
70976 .87982
                                                                              11891. .18653
/note="assembly_fragment"
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/note="TCR V&agr"
join(58. .109,340. .>716)
/gene="TCR V alpha"
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/db_xref="taxon:9606"
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LOCUS S63879
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TITLE
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MEDLINE
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SOURCE
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| AF58079 HTLV-2 isolate FOR2
| AF058080 HTLV-2 isolate FOR3
| AF058081 HTLV-2 isolate P1 e
| AF058082 HTLV-2 isolate P1 e
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1 (bases 1 to 1318)
Jantzer, P. U. and Schendel, D. J.
Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of secondary immune response
                                                                                                                                                                                                                                                                                                   08-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology, Goethestr. 31, D- 80336 Munich, FRG Location/Qualiflers
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                                                                                                                                                                                                                                                                                                   DEFINITION H. Sapiens mRNA for rearranged TCR junctional sequences. ACCESSION X98410
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Gaps: 0
Percent Identity: 100.000
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/protein_id="CAA67057.1"
/db_xref="GI:1770561"
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/isolate="patients 22 and 26"
/db_xref="taxon:9606"
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97.60
97.60
97.60
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A93131
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08-881509-9 x HSTCRJUNC
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                                        gb_vil:AF058079
gb_vil:AF058080
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ACCESSION
VERSION
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KEYWORDS
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AUTHORS
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9b_in3:PHE133553
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9b_htg22:AL360083
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gb_htg20:AL160052
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gb_htg4:AC013484
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9b_pr6:HS394p21
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9b_pr7:HSU14029
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em_bal:AP002548
9b_vi2:HTLVIIGP1
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gb_bal:AE002259
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9b_htg15:
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                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clonal expansion of myelin basic protein-reactive T cells in patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 87)
Vandevyver,C., Mertens,N., van den Elsen,P., Medaer,R., Raus,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / note="Partial TCRVA (1. .15), TCRNA (16. .18), TCRJA (19. .75), partial TCRCA (76. .87)" (19. .75), partial TCRCA (76. .87)" (40. xref="GDB:G00-120-404" (40. xref="GDB:G00-120-404" (40. xref="GDB:G00-120-404")"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (clone NSI-F4) T cell receptor alpha chain (TCRA) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                    4.417 Gaps: 0
92.308 Percent Identity: 84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L42801.1 GI:853662
T cell receptor alpha.
Homo sapiens (clone: NSI-F4) cDNA to mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunol. 25 (4), 958-968 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 CysLeuAlaProSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                                                                                                                               /note="unnamed protein product"
                                                                                         T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                 /translation="CLVLSGSARQLTF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                              /protein_id="CAB69531.1"
/db_xref="G1:6741521"
                                                                                                                                                                              /organism="unidentified"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: A93131 from: 1 to: 39
                                                                                                                                                                                             /db_xref="taxon:32644"
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9
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/map="14q11.2"
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                                                             (bases 1 to 39)
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                                                                                Schendel, D.J.
          unidentified
                                               unclassified
                           unidentified
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95255419
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KEYWORDS
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em: EMBL: SW:, SWISSPROT: TT: TREMBL: Wp:, WORNPEP; Information to the WORNPEP database can be found at the WORNPEP database can be found at the WORNPEP database.

Was generated from part of bacterial clone contigs of human was generated from part of bacterial clone contigs of human mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr20

http://www.sanger.ac.uk/HGP/Chr20

http://www.sanger.ac.uk/HGP/Chr20

park Cancer Institute by the group of pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  together with a note of the overlapping clone name. Note that the together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, so as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
RRP11-65K20 It may be shorter because we sequence overlapping
sections only once, except for a 100 base overlap.
The true left end of clone RP5-1167H4 is at 20504 in this sequence.
The true right end of clone RP1-380D15 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (30-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk clonerequest@sanger.ac.uk clonerequest@sequence version replaced gi:9542799.

On Aug 1, 2000 this sequence version replaced gi:9542799.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AL359534 20603 bp DNA PRI 07-SEP-2000 Human DNA sequence from clone RPII-65K20 on chromosome 20 Contains part of a gene for a novel protein similar to vacuolar AFPase isoform VA68. Contains ESTs, STSs and GSSs, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 20603)
                                                                  /translation="YFCAEASGSARQLTFGSGTQLTVLPDIQK"
                                                                                                                                                                                                                                                                                                Length: 14
Gaps: 0
Percent Identity: 71.429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: HUMTCRACG from: 1 to: 87
/protein_id="AAA80964.1"
/db_xref="GI:853663"
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HTG; ATPase.
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Location/Qualifiers

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Percent Identity: 69.231
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14864. .15063
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
/tissue_type="synovial fluid"
/clone="AV3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
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                                                                                                                                  16381. .16558
/note="LTR33 re
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08-881509-9 x AL359534
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match: ESTs: Em:N74518 Em:AA418630 Em:R43762 Em:AI797879
Em:AM658428 Em:AA1457682 Em:AI033751 Em:AI669434 Em:H23200
Em:H18658 Em:AA576047 Em:AI554929 Em:AA244669 Em:A1142863
Em:AI243726 Em:AIZ72715 Em:AA836368 Em:AI37906 Em:D19704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
/product="ba65K20.1 (novel protein similar to vacuolar
ATPase isoform VA68)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5504. .5637
//note="LiMBB repeat: matches 5693. .5828 of consensus"
//note="LiMBB repeat: matches 4906. .6168 of consensus"
//note="LiMBB repeat: matches 4906. .6168 of consensus"
//note="LiMBB repeat: matches 5821. .6171 of consensus"
//49. .7459. .7459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1844. .2310
/note="LIPA3 repeat: matches 5680. .6146 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8178. 9258
70cte="Lipba repeat: matches -1549. .-412 of consensus"
9246. 10818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10816. .11110
//orde="Aluy repeat: matches 1. .300 of consensus"
//orde="Lip91 repeat: matches 1272. .3677 of consensus"
//orde="Lip91 repeat: matches 4337. .5791 of consensus"
//orde="Lip91 repeat: matches 4337. .5791 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14024. 14063
/note="20 copies 2 mer at 80% conserved"
14092. 14463
/note="LiPBl repeat: matches 5783. 6155 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="LIPBa repeat: matches -279. .1272 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3411. .3515
/note="LLM1 repeat: matches 5536. .5642 of consensus"
                                                                                                                                                                                                                                                                   repeat: matches 2320. .2750 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7249. 7459
/note-"MITIE repeat: matches 344. 568 of consensus"
7702. 7882
/note-"L2 repeat: matches 2530. 2693 of consensus"
                                                                                                                                                                                                                                                                                                   /note="L2 repeat: matches 1840. .2015 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2886. .3012
/note="FLAM_C repeat: matches 1. .123 of consensus"
                                                                                                                                                                                                                                /note="MIR repeat: matches 35, .228 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1665. 5017
Mote="THE1B repeat: matches 1. 364 of consensus"
                                                                                                                                                                                                                                                                                                                                                     complement(join(1450. .1559,1658. >1808))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(join(1450. .1559,1658. .1808))
/gene="bA65K20.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         561. 1658
note-"49 copies 2 mer ca 76% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2313. 2356
//note="22 copies 2 mer aa 77% conserved"
                                                                                                                                                                                                  /note="match: STS: Em:HS499G10S"
678. .866
                                                                                                                             /note="match: GSS: Em:AQ389996"
101. .511
                                                                                                                                                            /note="match: GSS: Em:AQ805436"
106, .603
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/db_xref="taxon:9606"
                                                                                         /clone_lib="RPCI-11.1"
82. .465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(1485. .1490)
/gene="bA65K20.1"
                                                      /chromosome="20"
/clone="RP11-65K20"
                                                                                                                                                                                                                                                                                                                         complement(1450)
                                                                                                                                                                                                                                                                                      .1438
                                                                                                                                                                                                                    .866
                                                                                                                                                                                                                                                                   /note="L2
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17493. .17590
/note="MER20 repeat: matches 123. .212 of consensus" complement(1719. .1795)
18041. .18344
/note="Malvi repeat: matches 1. .305 of consensus" complement(19576. .19895)
/note="match: GSS: Em:AQ012075"
/note="match: GSS: Em:AQ012075"
/note="match: GSS: Em:AQ012075"
/note="LIMB7 repeat: matches 6025. .6169 of consensus" complement(19576. .19895)
/note="LIMB7 repeat: matches 6025. .6169 of consensus" content and also consensus and content and consensus and content and consensus and consensus and consensus and also consensus and a
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens patient CS-1 clone AV3 T cell receptor alpha chain
AF043876
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14630. .14756
/note="L2 repeat: matches 2620. .2750 of consensus"
14827. .15221
                                                                                                                                                                                                                                                                                                               /note="MER20 repeat: matches 16, .217 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTR33 repeat: matches 16. .201 of consensus" .16926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anotes"MLT1B repeat: matches 2. .363 of consensus"
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Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Selective accumulation of related CD4+ T cell clones in the
Synovial fluid of patients with rheumatoid arthritis
J. Immunol. 161 (8), 4428-4436 (1998)
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Align seg 1/1 to: S69140 from: 1
                                    Quality:
                                                 Ratio:
                                                                 Percent Similarity:
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                                      /note="Contains the 3' end of the TCRAV, the n, and the 5' end of the TCRAJ."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L. Direct Submission 1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ARU43877 51 bp mRNA PRI 11-NOV-1998
Homo sapiens patient CS-1 clone AV4 T cell receptor alpha chain
CDR3 (TCRA) mRNA, partial cds.
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/product="I cell receptor alpha chain CDR3"
/prodein_id="AAC72677.1"
/db_xref="G1:3859384"
/translation="YFCAVRPSGSARQLTFG"
                                                                                   /product="T_cell receptor alpha chain CDR3"
/protein_id="AAC72676.1"
/db_xref="GI:3859382"
                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 73.333
                                                                                                                                        /translation="YECAVRPSGSARQLTFG"
13 c 14 g 16 t
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/db_xref="taxon:9606"
/tissue_type="synovial fluid"
/clone="AV4"
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<1. .>51
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                                /gene="TCRA"
/gene="TCRA"
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3.962
86.667
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LOCUS AF043877
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 98)
Mohapatra,S.S., Mohapatra,S., Yang,M., Ansari,A.A., Parronchi,P., Maggi,E. and Romagnani,S.
Molecular basis of cross-reactivity among allergen-specific human T cells: T-cell receptor V alpha gene usage and epitope structure luminology 81 (1), 15-20 (1994)
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/note="This sequence comes from Fig. 3b; Protein sequence
is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                   DOCUS S69140 98 bp mRNA FALL COURS S69140 TCR V alpha=T-cell receptor alpha-chain [allergen-specific] [human, perintion TCR V alpha=T-cell receptor alpha-chain allood, mRNA Partial, grass-sensitive individual VI 19, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144562] from the original journal article. This sequence comes from Fig. 3a.

Location/Qualifiers
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27 c 20 g 28 t
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/protein_id="AAB30244.1"
/db_xref="G1:545974"
                                                                                                                                                                                                             /note="T-cell receptor alpha-chain"
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78.571 Percent Identity: 71.429
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                                          Percent Identity: 73.333
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/db_xref="taxon:9606"
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08-881509-9 x AF043877
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S69139.1 GI:545971
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LOCUS HSU40776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="METLLEVLSGTLLMQLTWVRSQQPVQSPQAVILREGEDAVINCS
SSKALYSVHWYROKHGEAPVFLMILLKGGEQKGHEKISASFNEKKQQSSLYLTASQLS
YSGTYRCGTASGSARQLTFGSGTQLTVLPDIQNPDPAVYQL"
                                                                                                                                  DEFINITION TCR V alpha = T in Dr DNA

DEFINITION TCR V alpha = T in Dr DNA

Genomic Mutant, 716 nt].
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DEFINITION TCR V alpha-r-cell receptor alpha-chain {allergen-specific} [human, grass-sensitive individual VI 53, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="This sequence comes from Figure 4; conceptual translation presented here differs from translation in
                                                                                                                                                                                                                                                                                                                                                                                                      GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 63879] from the original journal article. This sequence comes from Figure 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/product="" cell receptor variable alpha chain"
//protein_id="AAB209911"
/db_xreff="GI:238693"
                                                                                                                                PRI
1 TyrCysLeuAlaProSerGlySerAlaArgGlnLeuThrPhe 14
                     4.167 Gaps: 0
85.714 Percent Identity: 71.429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="TCR V&agr"
join(58. .109,340. .>716)
/gene="TCR V alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: S63879 from: 1 to: 716.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="TCR V alpha"
                                                                                                                    716 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Publication"
                                                                                                                                                                                    S63879.1 GI:238692
                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                     Homo sapiens
                                                                  seq_name: gb_pr8:S63879
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08-881509-9 x S63879
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                                                                                                                        863879
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ORIGIN
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Molecular basis of cross reactivity among allergen-specific human rels. T-cell receptor V alpha gene usage and epitope structure immunology 81 (1), 15-20 (1994)
                                                                                                 1 (bases 1 to 98)
Mohapatra, S.S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P.,
                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human T-cell receptor alpha chain (TCRAV2S1J22) mRNA, partial cds.
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T-cell receptor usage by anti-melanoma specific cytotoxic tumor-infiltrating lymphocytes. Detection of dominant tumor-specific T-cell clones by single strand conformational Oppublished (1995)

Compublished (1995)
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Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.
1 (bases 1 to 214)
                                                                                                                                                                                                                                                                           GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144561] from the original journal article. This sequence comes from Fig. 3a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /exception="Protein Inger than coding region shown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-DEC-1995
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/protein_id="AAB30243.1"
/db_xref="G1:545972"
/translation="DSATYFCAAPTGTASKLTFGTGTRLQVTLDIQN"
human peripheral blood grass-sensitive individual VI 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TcR V alpha"
/note="This sequence comes from Fig. 3b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="T-cell receptor alpha-chain"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="TcR V alpha"
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                                                                                                                                                    Maggi, E. and Romagnani, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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96028: cort
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69432: cont
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                                                                                                                                                                                                                                                                                                                                                                      /product="T-cell receptor alpha chain"
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/protein_id="AAA83012.1"
/protein_id="T11039712.1"
/branslation="SIYSNG7NEDGRFTAQLNKASQYVSLLIRDSQPSDSATYLCAVN /translation="SIYSNG7NEDGRFTAQLNKASQYVSLLIRDSQPSDSATYLCAVN SGSARQLIFGSGTQLTVLPDIQNPDPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162356)
Kurnick,J.T., Ihara,A., Pervaiz,S., Pandolfi,F., Van,Den Elsen P., Waitkus,R., Boyle,L.A., Hishli,M. and Andrews,D.M.
Direct Submission
Submitted (16-Nov-1995) James T. Kurnick, Pathology Research
Laboratory, Massachusetts General Hospital, 149 East 13 St.,
Charlestown, MA 02129, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, Submitted (09-AUG-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk requests: clonerequest@sanger.ac.uk on Aug 11, 2000 this sequence version replaced gi:9211825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-2000
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LOCUS AL136380 162356 bp DNA PF5-88207 map p33-34.2, ***
DEFINITION Homo sapiens chromosome 1 clone RP5-88207 map p33-34.2, ***
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; L0875; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads consensus quality: 154851 bases at least Q40
                                                                                                                                                                                                                              /cell_type="cytotoxic T-cell lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ***, 19 unordered pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.00 Length: 13
4.455 Gaps: 0
84.615 Percent Identity: 76.923
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                                                                                                                                                                                                                                                                                                                                   /note="V alpha 2.1 J alpha 22"/codon_start=1
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Web site: http://www.sanger.ac.uk
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                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45 g
                                                                                                                                                                                                                                                                                /gene="TCRAV2S1J22"
                                                                                                                                                                                                                                                                                                                      /gene="TCRAV2S1J22"
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                                                                                                                                                                                                                   /clone="MU 57"
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08-881509-9 x HSU40776
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JOURNAL
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                         AUTHORS
                                                                                    JOURNAL
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                                                                                                                                            FEATURES
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Consensus quality: 157434 bases at least Q30 consensus quality: 159115 bases at least Q20 consensus quality: 159115 bases at least Q20 lnsert size: 160556; sum-of-contigs Insert size: 164066; agarose-fp quality coverage: 4.59x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51 26850; gap of 100 bp in length 37556; contig of 10706 bp in length 57 37656; gap of 100 bp 100 bp
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134647: contig of 25400 bp in length
14747: gap of 100 bp
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96129 109147: contig of 13019 bp in length
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139480 155287: contig of 15808 bp in length
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75257: contig of 5725 bp in length
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10062 17452; contig of 7391 bp in length
17453 17552; gap of 100 bp
17553 26750; contig of 9198 bp in length
26751 26850; gap of 100 bp
26851 2856; contig of 10706 bp in length
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10062 ...17451

/note="assembly_fragment:00878

fragment_chain:1"

17553 ...26750

/note="assembly_fragment:01422

fragment_chain:1"

26851. .37556
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/note="assembly_fragment:00284
fragment_chain:1"
4190. .9061
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fragment_chain:1"
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/note="assembly_fragment:00403
fragment_chain:4"
69533. .75257
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75358. .79658
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Patent: EP 0816496-A 07-JAN-1998;
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Sequence 1 from Patent EP0816496.
A93127
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Schendel, D.J.
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Ratio: 4.083
Percent Similarity: 85.714
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ATNDYITWYQQPPSQGFRFIIGGYKRKVINEVASLEIPADRKSSTLSLPRVSLSDTAV
YYCLVGGSARQLIFGSGTQLTVLPDIQNPDPAYYQLRDSKSSDKSVCLFIDFDSQTNV
SQSKDSDYYITDKTVLDMRSNDFKSNSAVAMSNKSDFACANAFNNSIIPEDTFFPSPF
SSCDVKLVEKSFFTDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLMSS"
                                                                                                                                                                                                                                                                 /translation="MRQVARVIVFLTLSTLSLAKTTQPISMDSYEGQEVNITCSHNNI
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DOE Joint Genome Institute and Stanford Human Genome Center.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 37141)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (21-MAR-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Greek, CA 94598, USA
4 (bases 1 to 37141)
DOE Joint Genome Institute and Stanford Human Genome Center.
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On Mar 21, 2000 this sequence version replaced gi:7021680.
Draft Sequence Produced by DOE Joint Genome Institute
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Quality: Phrap Quality >-40 100% of Sequence;
Estimated Total Number of Errors is 0.
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/protein_id="CAB69529.1"
                                                                     /organism="unidentified"
/db_xref="taxon:32644"
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BOEHRINGER MANNHEIM GMBH (DE)
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DOE Joint Genome Institute.
Direct Submission
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Percent Similarity: 92.857
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This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 human chromosome 1, constructed by the Sanger Centre Chromosome 1 hutp://www.sanger.ac.uk/HGP/Chri Connot at the Roswell Park 654H19 is from the library RPCI-4 constructed at the Roswell Park Cancer institute by the group of pieter de Jong. For further cancer institute by the group of pieter de Jong. For further Location/Quallfiers
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AL Cambidestion
AL Cambidestion
Submitted (03-SEP-1999) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On Jul 27, 1999 this sequence version replaced gi:5514763.
On Jul 27, 1999 this sequence version replaced gi:5514763.
On Jul 27, 1999 this sequence version replaced gi:5514763.
On Jul 27, 1999 this sequence version these are annotated as variations
Where differences are found these are annotated as variations
where differences are found these are annotated as variations
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
number given in the feature table with their source databases:
on the WORMPEP database can be found at
http://mxm.oncor.ac.uk/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/noriane/norian
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AC020943 from: 1 to: 37141
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Gaps: 0
Percent Identity: 61.538
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                                                                                                                                                                                                            7294 g 11764 t
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/db_xref="taxon:9606"
/chromosome="1"
                                                                  /organism="Homo sapiens"
                                                                                                    /db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                       /clone="LLNLF-108H7"
Location/Qualifiers
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AL049745.9 GI:5596759
HTG; CpG Island.
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                                                                                                                                                                                                                   7134 C
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Ratio: 4.000
Percent Similarity: 92.308
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3716. .9982
/note-"LIMB3 repeat: matches 5897. .6182 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LIMB5 repeat: matches 5714. .5848 of consensus"
                                                                                         116. .189
/note="AluSp/q repeat: matches 243. .301 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5598. 5744
/hote="AluSq/x repeat: matches 1. .145 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note-"12 repeat: matches 2341. .2708 of consensus"
3100. .13411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16825, .17112
/note="AluJb repeat: matches 8. .296 of consensus"
17611. .17726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="L2 repeat: matches 2062. .2215 of consensus"
519. .7185
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9716. .9982
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14572. .14729
                                                                                                                                                                                                       /note="MLT1J repeat: matches 478. .501 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7137 .11432
7note="AluSp repeat: matches 1. .295 of consensus"
11540. .11839
                                                                                                                                                                                                                                                                                                                                                                                                                                                              4728. 4861
/note="FLAM_A repeat: matches 2. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Alusx repeat: matches 1. .296 of consensus"
8576. .8860
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                                                                                                                                                               1219. .1366
/note="L2 repeat: matches 2589. .2748 of consensus"
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7257. .7440
                                                                                                                                                                                                                                                                                              /note="lusx repeat: matches 1. .297 of consensus" 1698. .2155
                                                                                                                                                                                                                                                                                                                                                                                                                                  1422. .4720
/note="AluSx repeat: matches 1. .300 of consensus"
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mote="MIR repeat: matches 53. .260 of consensus"

mote="MIR repeat: matches 53. .260 of consensus"

1929. .8181
                                                                                                                   534 .845
/hote="AluSc repeat: matches 1. .307 of consensus"
                                                                                                                                                                                                                                                       /note="MITLJ repeat: matches 1. .478 of consensus" 2203. .2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14572. .14729
/note="FAM repeat: matches 1. .159 of consensus"
                                                              /note="Alu repeat: matches 2. .62 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                               /evidence=not_experimental
/map="p31.1-33"
/clone_lib="RPCI-4"
/clone="RP4-654H19"
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/note="CpG island"
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/note="FLAM_C repeat: matches 2. .117 of consensus"
/note="AluJo repeat: matches 1. .312 of consensus"
/note="match: 5' EST: Em:R91335 clone 195181; Paired with
EST Em:R91293 matching this clone; match: 3' EST:
Em:R91293; Paired with EST Em:R91335 matching this clone"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            //octe="Aluy repeat: matches 1. 310 of consensus"
27940. 30182
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7.00te="Liner repeat: matches 6120. .6168 of consensus" 24372. .27627  
7.00te="Liner repeat: matches 2030. .6155 of consensus" 27628  
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/note="MER30 repeat: matches 117. 175 of consensus" 21727. 22039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="LlMB2 repeat: matches 5768. .6120 of consensus"
23566. .23856
                                                                                                                                                                                                                                                         19669. 19834. "Atun EST Em:R91335 matching this c. 700te-"Alusq repeat: matches 126. .291 of consensus" 19979. .20044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                //note="match: GSS: Em:AQ517971"
33434. 33650
/note="Match: repeat: matches 47. .262 of consensus"
34737. 35046
/note="Alusx repeat: matches 1. .310 of consensus"
59526. 36218
/note="Alux repeat: matches 1. .293 of consensus"
36537. 36837 repeat: matches 32. .308 of consensus"
/note="Alux repeat: matches 32. .308 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MIR repeat: matches 166. .256 of consensus" 20547. .20859 //note="Alucx repeat: matches 1. .306 of consensus" 21006. .21309 //note="Alucx repeat: matches 1. .306 of consensus" //note="Alucx repeat: matches 1. .306 of consensus" 21478. .21617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alusx repeat: matches 1. .312 of consensus"
22040. .22159
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22376. .22636
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/note="FRAM repeat: matches -6. .165 of consensus"
33095. .33387
/note="match: GSS: Em:AQ355375"
33101. .33433
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/note="12 repeat: matches 2455. .2659 of consensus"
38141. .38437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MIR repeat: matches 2, .262 of consensus" 22637, .23098
/note="match: GSS: Em:AQ237932" 23210, .23565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note-"AluSx repeat: matches 1. .301 of consensus"
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/note="Alur repeat: matches 1. .297 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                      /note="33 copies 2 mer aa 70% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                          20132. .20212
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 135935)
                                                                                                                  /note="AllSgl repeat: matches 1. .303 of consensus" 41816 .41867 /note="LIMA9 repeat: matches 6235. .6285 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-A0G-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Aug 25, 2000 this sequence version replaced gi:9801504.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AL391003 135935 bp DNA HTG 23-AUG-2000
DEFINITION Homo sapiens chromosome 1 clone RP11-205P11, *** SEQUENCING IN
PROGRESS ***, 29 unordered pieces.
                  /note="Aluyo repeat: matches 13. .299 of consensus" 39983. .40251
/note="Alusx repeat: matches 15. .297 of consensus" 41387. .41678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5 Sequencing vector: plasmid; LO8752; 100% of reads Chemistry: Dye-terminator Big Dye; 40% of reads Chemistry: Dye-terminator ET-amersham; 59% of reads quality: 119874 bases at least Q40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Consensus quality: 125595 bases at least 030 Consensus quality: 129421 bases at least 020 Consert size: 133135; sum.of-contigs Insert size: 1614949; 9.5% error; agarose-fp Quality coverage: 3.50x in 020 bases; sum-of-contigs Quality coverage: 2.89x in 020 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 29 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: HSJ654H19 from: 1 to: 117493
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                                                                                                                                                                                                                                                          Percent Similarity: 91.667 Percent Identity: 75.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10859 TGCTGGCACCACAGGGATCCATCAGAAGGTTGACC 30824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 CysLeuAlaProSerGlySerAlaArgGlnLeuThr 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: SC
Web site: http://www.sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ....- Summary Statistics
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39317. .39614
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                                                                                                                                                                                                                                                  48.00
                                                                                                                                                                                                                                                                                                                                                                  08-881509-9 x HSJ654H19/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_htg22:AL391003
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                                                                                                                                                                                                             alignment_scores:
Quality:
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
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100 bp

3474 3573: gap of

/note="Alujb repeat: matches 1. .280 of consensus"

. .38925

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88163 88262: gap of 100 bp 88263 92173: contig of 3911 bp in length 92274 92273: gap of 100 bp 92274 95649: contig of 3376 bp in length
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                                       10237 10336; gap of 100 bp in length 10337 12524; contig of 2188 bp in length 1252 12634; gap of 100 bp 16625 12188; contig of 9164 bp in length
                                                                                                                                                                                                                                                                                                                                          77623 27722: gap of 100 bp
27723 30841: contig of 3119 bp in length
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38698 41812: contig of 3115 bp in length
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21889 24154: contig of 2266 bp in length
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27622: contig of 3368 bp in length
10236: contig of 6663 bp in length
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/note="assembly_fragment:00313"
24255. .27622
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/clone_lib="RPCI-11.1"
1. .3473
//note="assembly_fragment:00103"
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/db_xref="taxon:9606"
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41913 51135: cont
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2817 others
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Gaps: 0
Percent Identity: 75.000
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95750. .98061

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108701. 119555
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125792. .129898
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                                                                 38698. .41812
/note="assembly_fragment:00503"
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             27723. .30841
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Percent Similarity: 91.667
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Len | Documentation | 1318 | X98410 H.sapiens mRNA for rear | 134 | A93127 Sequence | from Patent | 995 | AL144658 Anopheles gambiae STS | 37751 | 1283864 Mycobacterium tubercul | 174788 | AP000755 Homo sapiens chrome | 185286 | AC016721 Homo sapiens chrome | 186787 | AC07357 Homo sapiens chrome | 186787 | AC07357 Homo sapiens chrome | 127447 | AC06344 Homo sapiens PAC cl | 157417 | AC06344 | AC06344 | AC06344 | AC06344 | AC06344 | AC06344 | A
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AC019767 Drosophila meLanogas
AC018624 Mus musculus chromc
AC068502 Homo sapiens chromc
AC068503 Homo sapiens chromc
AC069303 Homo sapiens chromc
AC069099 Homo sapiens chromc
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AC06903 Homo sapiens chromc
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AC079128 Oryza sativa chromc
AC079128 Oryza sativa chromc
AC019652 Drosophila melanoga
AC019648 Drosophila melanogas
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AC019671 Arabidopsis thaliana
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AL067687 Homo sapiens chromc
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| AF079139 Streptomyces venezuel
| AC005119 Drosophila melanogas
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AC002542 Human BAC clone CTE
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AC015947 Homo sapiens clone
AC024329 Homo sapiens clone
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                                                                                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Database length: -1736092196
Search time (sec): 3669.820000
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9b_pt27:AC06344
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| ACO24233 Homo sapiens chr
| ACO22528 Homo sapiens chr
| ACO15711 Homo sapiens chr
| ACO12531 Homo sapiens, cl
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J gene; junction; T cell receptor; TCR junctional sequence; V gene
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Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Prinates; Catarrhini; Hominidae; Homo.
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H.sapiens mRNA for rearranged TCR junctional sequences.
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Gaps: 0
Percent Identity: 100.000
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/codon_start=1
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/isolate="patients 22 and 26"
/db_xref="taxon:9606"
               1.0e+04
1.0e+04
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1.0e+04
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A93127
A93127.1 GI:6741516
               87.68
87.58
87.36
87.30
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Jantzer, P.
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08-881509-10 x HSTCRJUNC
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LOCUS A93127
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9b_htg10:AC024233
9b_htg9:AC022528
9b_htg5:AC015711
9b_pr3:AC012531
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                                                                                                                                                                                                                                                                                                                                                                                                     ATNDYITWYQOFPSGGPRFIIQGYKRKVYNBVASLFTPADRKSSTLSLPRVSLSDTAV
YYCLVGGSARQLTFGGGTQLTVLPDIQNPDPAVYQLRDSKSSDKSVCLFTDFDSQTNV
SQSKDSDVYITDKTVLDMRSMDFKSNSAVANSNKSDFACANAFNNSIIPEDTFFPSPE
                                                                                                                                                                                                                                                                                                                                                                     /db_xref="G1:6741517"
/translation="MRQVARVIVFLTLSTLSLAKTTQPISMDSYEGQEVNITCSHNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anophales gambiae STS SP6 end of clone 09C07 of NotreDamel library from strain PEST of Anophales gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (16 FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr. Roux, Paris 75015, France
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culidae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-FEB-2000
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2 (bases 1 to 995)
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSCDVKLVEKSFETDTNLNFONLSVIGFRILLLKVAGFNLLMTLRLWSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.083 Gaps: 0
92.308 Percent Identity: 92.308
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                                                                                                                                                                                                                                                                                                            /note="unnamed protein product"
                                                                                                                            T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
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                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB69529.1"
                                                                                                                                                                                                                        /organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                                         Location/Qualifiers
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365 c
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Schendel, D.J.
                                 unidentified
                                                    unidentified
unclassified
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08-881509-10 x A93127
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BASE COUNT 3
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tuberculosis sequencing and mapping teams, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA Unite de Genetique Moleculaire Bacterienne, Institut Pasteur, 28 rue du Docteur Roux, 75724 Paris Cedex 15, France E-mail: parkhill@sanger.ac.uk on Jun 27, 1998 this sequence version replaced 91:1781088.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/M_tuberculosis/) CDS have been renumbered from the original cosmid submissions but the old gene designations are in brackets after the new gene numbers Gene prediction was based on a Hidden Markov Model of TB genes implemented in TBparse (Krogh) supplemented with visual inspection of positional base preference in codons, especially where there is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mycobacceilum.

(dases 1 to 37751)

(cole, S.T., Brosch, R., Parkhill, J., Garnier, T., Churcher, C.,

Cole, S.T., Brosch, R., Biglmeier, R., Gas, S., Barry Ill, C.E.,

Harris, D., Gordon, S.V., Eiglmeier, R., Gas, S., Barry Ill, C.E.,

Tekaia, F., Badcock, K., Basham, D., Brown, D., Chillingworth, T.,

Tekaia, F., Davles, R., Pellwell, T., Gentles, S.,

Hamlin, N., Holroyd, S., Hornsby, T., Jagels, K., Krogh, A., McLean, J.,

Moule, S., Murphy, L., Oliver, S., Osborne, J., Quail, M.A.,

Rajandream, M.A., Rogers, J., Rutter, S., Seeger, K., Skelton, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis H37Rv complete genome; segment 159/162.
283864 AL123456
283864.1 GI:3261687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (11-JUN-1998) Submitted on behalf of the Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Sqares, R., Sulston, J.E., Taylor, K., Whitehead, S. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Details of M. tuberculosis sequencing at the Sanger Centre are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Firmicutes, Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Erratum:[[published erratum appears in Nature 1998 Nov 12:396(6707):190]]
2 (bases 1 to 37751)
                                                                                                                                                                                                                                              3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to reverse of: CNSO1HNL from: 1 to: 995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BCT
                                                                                                                                                                                                                                                                                                                                                                                           Length: 13
Gaps: 0
Percent Identity: 61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 TyrCysLeuValGlyArgSerAlaArgGlnLeuThrPhe 13
                                                               /organism="Anopheles gambiae"
                                                                                                                                                                                                                                              269 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete genome sequence
Nature 393 (6685), 537-544 (1998)
98295987
                                                                                                                                                                                     /clone_lib="NotreDame1"
                                                                                                                     /db_xref="taxon:7165"
/clone="09C07"
Location/Qualifiers
                                                                                                                                                                                                                  /note="end: SP6"
222 c 216 g
                                                                                               /strain="PEST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37751 bp
                                                                                                                                                                                                                                                                                                                                                                                                                              Ratio: 3.769
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-881509-10 x CNS01HNL/rev
                                                                                                                                                                                                                                                                                                                                                                                                       49.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_ba2:MTCY1A6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkhill, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Squares, S.
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Ratio:
                                                                                                                                                                                                                                                        285
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/note="Rv3830c, (MTCY01A6.39), len: 209. Probable transcriptional regulator, similar to TCMR_STRGA P39885 tetracenomycin c transcriptional repressor (226 aa), fasta scores, opt: 255, E(): 1.9e-11, (33.7% identity in 202aa overlap). Contains possiblehelix-turn-helix motif from aa 34-55 (+4.97 SD)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MVRPPQTARSERTREALRQAALVRFLAGGVEATSAEQTAEDDAGV
SLRTFYRHFRSKHDLLFADVDAGLHWFRAALDARPADESIIDSVQAAIFSFPYDVDAV
TKIASLRRGELEPSRIVRHWREVEADFADAIQAQLRRRNCDIRGAPDARLHIAVTARC
VAAAVFGAMEAWMLGSDRSLGELARVCHVALESLRVGISDTWTLIVSS"
749. 1231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mysllyhaalgyvyjgmivssnpkyftrpaggswfslpecyyyv
Vgiasialgwyfnirfyqqyahgaanplwgpgswaeyyrlmfnpaassagdyytian
Villplestydgyrrglrrpwlyfysslftsfafafafyfatierqhrhersratyga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation-"MAMNLLHRRHCSSAGWEKAVANQLLPWALQHVELGPRTLEIGPG
                    CAUTION: In some cases we may not have predicted the correct initiation codon. Where possible we choose an initiation codon (atg, gtg, or ttg) which is preceded by an upstream ribosome binding site sequence (optimally 5-13bp before the initiation codon). If this cannot be identified we choose the most upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGATLGALLGELTASLTAVEVDNSMVERLNRRYGGRARITRGDGTQTGLEDDHFTSVVC
FTMLHHVASAQLQDQLFAEAYRVLQPGGVFAGSDGVPSLPFRLIHIADTYTPIAPADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Rv3833, (MTCY01A6.36c), len: 263. Possible
transcriptional regulator, similar to e.g. YFIE_BACSU
an increase in the observed/expected third position \mathsf{G}+\mathsf{C}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Rv3832c, (MTCY01A6.37), len: 191. Unknown."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Rv3831, (MTCY01A6.38c), len: 160. Unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein Rv3830c"
/protein_id="CAB06211.1"
/db_xref="G1:1781127"
                                                                                                                                                                                                                                               /organism="Mycobacterium tuberculosis"
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/transl_table=1
/product="hypothetical protein Rv3832c"
/protein_d="CA806209.1"
/db_xref="GI:1781125"
                                                                                                                                                                                                                                                                                                                                                          /organism="Mycobacterium tuberculosis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="hypothetical protein Rv3831"
/protein_id="CAB06210.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref-"SPTREMBL:P96248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="G1:1781126"
/db_xref="SPTREMBL:P96247"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(1228. .1803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="Rv3832c"
complement(1228. .1803)
/gene="Rv3832c"
                                                                                                                                                                                                                                                                                                         /db_xref-"taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref-"taxon:1773"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(48. .677)
/gene="Rv3830c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(48. .677)
/gene="Rv3830c"
                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                       /strain="H37Rv"
                                                                                                                                                                                                                                                                               /strain="H37Rv
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749. .1231
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="Y1A6"
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/note="Rv3833,
                                                                                                                                                                                                                                                                                                                                   .37447
                                                                                                                                                              initiation codon.
                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                source
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/note="Rv3834c, (MTCY01A6.35), len: 419. Seryl-trna
synthetase, similar eg to SYS_BACSU P37464 (425 aa), fasta
scores, opt: 1015, E(): 0, (39.3% identity in 425 aa
overlap); contains PS00179 Aminoacyl-transfer RNA
synthetases class-II signature 1"
                                                                                                                                                                                                                                                                                                                                                         HAGTWITPVNRAIWIPAGCWHOHKFHGHTQFHGVALDPORYRGGPATPTVLAVNPLMR
ELVIACSQADRTDTDEHHRMLAVLQDQLPTTSIREPLWYPSPTDRKLHHACALIADNL
TQPLTLQQIGGRIGVSQRTLSRLFSDELGWTFPQWRTOLRLQHALVLLAERHDVTSVA
SECGWATPSAFIDTYRQAFGHTPGQAAKPMAATRLTRLRRARDRR"
                                                                                                                                                                                                                                                                                         /db_xref="SPTREMBL:P96245"
/translation="MSBNSHHRLATTSLTLPPGARIERHRHPSHQIVYPSAGAVSVTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLTGRGALLQLGLLQLALKLAVDNGFVPTIPPVLVRPEVMVGTGFLCAHABEVYRVEG
BQZYLVGTSBYDLAGYHSGEILDLSRGPLRYAGWSGCFRREAGSHGKDTRGIIRVHOF
DKVEGFYYCTPADAEHEHERLLGWQRQMLARIEVPYRVIDVAAGDLGSSAARKFDCEA
WIPTQGAYRELTSTSMCTTFQARRLATFYRDASGKPQIAATLNGTLATTRMLVAILEN
HQRPDGSVRVPDALVPFVGFUFFVARRATFYRDASGKPQIAATLNGTLATTRMLVAILEN
P54722 hypothetical transcriptional regulator (314 aa), fasta scores, opt: 171, E(): 8.5e-05, (30.2% identity in 126 aa overlap). Contains probable helix-turn-helix motif from aa 165-186."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADSLRAEQKAASKSVGGASPEERPPLLRRAKĒLAEQVKAAEADEVEAEAAFTAAHLAI
SNVIVDGVPAGGEDDYAVLDVVGEPSYLENPKDHLELGESLGLIDMQRGAKVSGSRFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation-"MIDLKLLRENPDAVRRSQLSRGEDPALVDALLTADAARRAVIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVRRYLGTKFDPNSKFTISMLWPGDBAWROAGERRILGGLOSPGPNNOOLAFKGKVAD
IDQSKVWPAGTCLGIDATTNQPIDVPVDCAAPHAMEVSGTVNIJAERFPDALPSEPEDG
GFIKDACTRWTDAYLAPLKTTTLTLIYPTLTLPSWSAGSRVVACSIGATLGNGGWA
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LLLTPALGGLLIAGLVTAIPAVGRAPERLAGYIASNPVPSTGAKINASENRYASGDCLM
WPDGTPESAAIVSCADEHRFEVAESIDMRTFPGMEYGQNAAPPSPARTQOISEEQCEA
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LPAQQPVVTPTRPPESHAPASAAPAETQPPPPDAGAPPATGSPEATPPGPAEPAPG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="PS00179 Aminoacyl-transfer RNA synthetases
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                                                                                                                                                                                                    /product="hypothetical protein Rv3833"
/protein_id="CAB06208.1"
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/protein_id="CAB06206.1"
/db_xref="G1:1781122"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="CAB06207.1"
/db_xref="G1:1781123"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(2647. .3906)
/gene="serS"
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                                                                                                                                                                                                                                                              /db_xref="GI:1781124"
                                                                                                                                                                         /transl_table=11
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/transl_table=11
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/transl_table=11
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                                                                                                                                    /codon_start=1
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/gene="Rv3836"
5393. .5806
/gene="Rv3836"
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/qene="Rv3835"
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VERSION
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                /translation="mtvrmpporedelivsdaldlippeladamdnvvvlvanrhpqhe 
NLLGQYEGYALTERGSDYAGSLPDAITIYREALLDACDSEDEVVDQVAITVIHEVAHH 
FGIDDERLDQLGWRDEPAPGRGNPDLSAPDAMNGP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Homosa; 1 to 174788  
Hattori,M. Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Published Only in Database (1999) In press 2 (bases 1 to 174788)  
Hattori,M., Ishi,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujiyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y. Direct Submission on the teather of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted discovering to the DDBJ/EMBL/GenBank databases. Masahira Hattori, The Institute of Physical and Chemical Research (RIKRN), Genomic Sciences Center (GSC); 1-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattoriegac.tken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-42-778-9923, Fax:81-42-778-9924)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AP000756 174788 bp DNA HTG 14-SEP-2000 HOMO sapiens chromosome 11 clone RP11-720D4 map 11q14, WORKING DRAFT SEQUENCE, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-SEP-2000
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Quality coverage: 12.08x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Sep 15, 2000 this sequence version replaced g1:8118915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator ET-amersham; 100% of reads Assembly program: Phrapp; version 0.990329 consensus quality: 171368 bases at least 040 consensus quality: 172579 bases at least 030 consensus quality: 17326 bases at least 020
                                                                                                                                                                                              /note="PS00142 Neutral zinc metallopeptidases, zinc-binding region signature" complement(6001. 6699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: RIKEN Genomic Sciences Center(GSC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Identity: 81.818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      web site: http://hgp.gsc.riken.go.jp/
Contact: hattori@gsc.riken.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name: HumDraft11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens DNA, clone:RP11-720D4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: MTCY1A6 from: 1 to: 37751
/db_xref="SPTREMBL:P96242"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clone name: RP11-720D4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .----- Summary Statistics
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                                                                                                                                                             5672. .5701
/gene="Rv3836"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio: 4.700
Percent Similarity: 90.909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: gb_htg23:AP000756
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LOCUS AP000756 17
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Ratio:
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KEYWORDS
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Homo sapiens chromosome 2 clone RP11-327J6, WORKING DRAFT SEQUENCE, 19 unordered pieces.
10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment"
164988. 170558
/note="assembly_fragment clone_end:SP6 vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121965. .136845
/note="assembly_fragment clone_end:T7 vector_side:left"
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                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                   14881 bp in length
17017 bp in length
10425 bp in length
5971 bp in length
1422 bp in length
1382 bp in length
1126 bp in length
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                                                                                                                                                  bp in length
bp in length
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Percent Identity: 61.538
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172181. .173562
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154063. .164487
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94101. .121864
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                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                   136845 config of
153952 contig of
16487 contig of
170558 contig of
172080 contig of
173562 contig of
174788 contig of
                                                                                                                   contig of contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                      /chromosome="11"
/clone="RP11-720D4"
/map="11q14"
1. 62406
                                                                                                                                                       121864 contig of
                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                    Jocation/Qualifiers
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Tocus AC016721 185286 bp
                                                                                                                     62406
                                                                                                                                        94000
                                                                                                                                                                                                                                                                                                                                                                                       1. .174788
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08-881509-10 x AP000756/rev
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170659
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KEYWORDS

REFERENCE AUTHORS

COMMENT

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46 104451: contig of 11806 bp in length 152 104551: gap of unknown length 152 121910: contig of 17359 bp in length 11 122010: gap of unknown length 134398: contig of 12388 bp in length 199 13498: gap of unknown length 15877: contig of 23879 bp in length 178 158477: gap of unknown length 178 158477: gap of unknown length 178 158277: contig of 26809 bp in length 178 185286: contig of 26809 bp in length
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//note="assembly_name:Contig20"

12011. 134398

//note="assembly_name:Contig21"

//note="assembly_name:Contig21"

//note="assembly_name:Contig22"

158478. 185286

//note="assembly_name:Contig23"

54 a 32166 c 32604 g 58737 t 182
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31753. .38667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18481. .24477
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/note="assembly_name:Contig13" 46092. 53002
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62578. 71453
/note="assembly_name:Contig16"
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/note="assembly_name:Contig18"
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04552. .121910
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/note="assembly_name:Contig17"
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/note="assembly_name:Contig6"
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                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig8"
11728. .18380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig9"
                                                                                                                                                                                                                                                                                                                                                     3947. .6182
/note="assembly_name:Contig7
                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                     /clone="RP11-327J6"
                                                                                                                                                                                                                                                                                                                                                                                                                vector_side:left"
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92.308
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08-881509-10 x AC016721/rev
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Percent Similarity:
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                                                                                                                                                                                          Direct Submission
Submitted (04-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammallais Euthbria; Primates; Catarrhini; Hominidae; Homo.
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gap between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                              MO 63108, USA
On Mar 13, 2000 this sequence version replaced gi:7022633
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: plasmid; 19% Chemistry: Dye-primer ET; 81% of reads Chemistry: Dye-terminator Big Dye; 19% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 173248 bases at least 040 Consensus quality: 177028 bases at least 030 Consensus quality: 177028 bases at least 030 Insert size: 185Kb; agazose-fp Insert size: 185Kb; agazose-fp ouality coverage: 4.00 in 020 bases; agarose-fp Quality coverage: 4.00 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                              Center project name: H-M19327J06
Sequencing vector: M13, 81%
                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of 1052 bp in length
gap of unknown length
contig of 2694 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of unknown length
contig of 5345 bp in length
gap of unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length
contig of 2236 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown length
of 5997 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 6653 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7224 bp in length known length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 7075 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 6915 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 6911 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of 9375 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig of 8876 bp in length
gap of unknown length
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                                                                                                              The sequence of Homo sapiens clone Unpublished 2 (bases 1 to 185286)
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                              Homo sapiens
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71554
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                               ORGANISM
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08-881509-10.rge

9

DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

AUTHORS REFERENCE

JOURNAL REFERENCE AUTHORS

TITLE

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85419 85518: gap of 100 bp 85519 92962: contig of 7444 bp in length 92963 93062: gap of 100 bp 92963 93067: gap of 100 bp 100677 100776: gap of 100 bp 100777 110361: contig of 9585 bp in length 110362 110461: gap of 100 bp 110362 110461: gap of 100 bp 110362 110461: gap of 100 bp 120398 120497: gap of 100 bp 120398 120496: contig of 9336 bp in length 120398 120496: contig of 9143 bp in length 120498 120560: contig of 9143 bp in length
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29741 142154: contig of 12414 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156211 156310; gap of 100 bp
156311 169999; contig of 13689 bp in length
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170100 185820; contig of 15721 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         185821 185920: gap of 100 bp
185921 186787: contig of 867 bp in length.
                                                                                                                                                                                                                                                                                                          contig of 24076 bp in length
p of 100 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64006: contig of 3845 bp in length
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68134: contig of 4028 bp in length
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contig of 4705 bp in length
                                                                                                                                                                                                                       of 100 bp
contig of 1553 bp in length
of 100 bp
                                                                                                                                                                                                                                                                                                                                               82: gap of 100 bp
33676: contig of 1094 bp in length
                                                                                                                                                                                                                                                                                                                                                                                             o of 100 bp contig of 1010 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                           34886: gap of 100 bp
37514: contig of 2628 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114: gap of 100 bp 40126: contig of 2512 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p of 100 bp
contig of 3407 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p of 100 bp contig of 3416 bp in length
            3075: contig of 3075 bp in length
; gap of 100 bp
4344: contig of 1169 bp in length
                                                                                                                                                             5550; gap of 100 bp 6653; contig of 1103 bp in length
                                                                                            of 100 bp contig of 1006 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_fragment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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78256 85418: cont
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43734 47149: cont
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60061: cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40226: gap of
43633: cont
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8306: con
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4445 5450: con
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8407 32482: cor
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                                              3076 3175: gap of
3176 4344: co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E (bases 1 to 186787)

B Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Baderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boguslavkiy, L., Boukhgalter, B., Colangelo, M., Collins, S., Collymore, A., Castler, A., Cabagelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gago, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grart, G., Hagos, B., Heaford, A., Horton, L., Karatas, A., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Lakocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., MacGonald, P., Marquis, N., McBwan, P., McGurk, A., McKernan, K., McPara, S., McGarthy, M., McBwan, P., McGurk, A., McKernan, K., McHans, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., Spantos, S., Schauer, S., Sch
                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                 Homo sapiens chromosome 2 clone RP11-70708 map 2, WORKING DRAFT SEQUENCE, 30 unordered pieces.
                                                                                                  04-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert size: 192000; agarose-fp
Insert size: 183887; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 consensus quality: 1/2765 bases at least 0.30 consensus quality: 1/79967 bases at least 0.30 consensus quality: 182697 bases at least 0.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: M13; M77815; 100% of reads
                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 186787)
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
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                                                                                                                                                                                                                                                      HTG; HTGS_PHASE1; HTGS_DRAFT
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                                                                                                                                                                                                                    AC073557.2 GI:10567944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 186787)
                                                                            seq_documentation_block:
LOCUS AC073557 186787 bp
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                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                        human.
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TITLE JOURNAL

COMMENT

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85519, .92962
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alignment_scores:

Quality: 47.00 Ratio: 3.917 Percent Similarity: 92.308 alignment_block: 08-881509-10 x AC073557 ..

Gaps: 0 Percent Identity: 53.846

Length:

Align seg 1/1 to: AC073557 from: 1 to: 186787

1 TyrCysLeuValGlyArgSerAlaargGlnLeuThrPhe 13 |||||||::::||||:: |101773 TACTGTGTTTAGGCAATAGAGCTAAACAGATAACATTT 101811

seq_name: gb_in3:TSAJ9167

23-MAR-2000	iomatidae; and primates	Gibson, W.C. human pathogenic ruzi ool of Biological Read, Reistol nes inc		·			22-AUG-1994 synthase. ; Bacillaceae;	, Tognoni,A., Grandi,G., polypeptide highly
documentation_block: S TSAJ9167 2130 bp DNA INV SSION Trypanosoma sp. 188 rRNA gene, isolate K&A. SSION AJ009167 GI:4468770 ONDS 188 ribosomal RNA; 188 rRNA gene. Trypanosoma sp.	Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatida Trypanosoma. (bases 1 to 2130) Stevens, J., Noyes, H. and Gibson, W. The evolution of trypanosomes infecting humans and prin Mem. Inst. Oswaldo Cruz 93 (5), 669-676 (1998) 2 (bases 1 to 2130)		Location/Qualifiers 12130 /organism="Trypanosoma sp." /isolate="R&A" /strain="Leech" /db_xref="taxon:5696" /l>2130 /gene="18s rRNA" /product="18s rRNA" /product="18s ribosomal RNA subur	48 a 48 a tty:	TSAJ9167 to: TSAJ9167 from: 1 to	1yrvsteuvalttykrgserAlaArgGln 10 	seq_documentation_block: DCCUS BSPOIKET 7735 bp DNA BSPOIKET ACCESSION 3.35133 BERSION 235133.1 G1:510952 VERSION 235133.1 G1:510952 VERSION 235133.1 G1:510952 VERSION BACILIUS SUbtilis, ORGANISM Bacillus subtilis, Bacillus subtilis Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillus subtilis Bacteria: Losaes 1 to 2446)	, Piatti, M., Cuzzoni, A., Perani, P and Albertini, A.M. s subtilis large ORF coding for a
seq_documer LOCUS DECENITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL MEDLINE REFERENCE	AUTHORS TITLE JOURNAL MEDLINE REFERENCE AUTHORS TITLE JOURNAL	FEATURES SOURCE IRNA	BASE COUNT ORIGIN alignment_scores:	alignment_block: 08-881509-10 x Align seg 1/1	• •	seq_document LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOUNCE ORGANISM	

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GDRKPLKISVPTYPFAKERYWISVPERKTSYVNHILHELVHRYBDPTSSVFTG
FPETASHWYQGOKILDGVAYLEMAREAAEKAAGDLDGEGRVVSLKDIVWWRPITIES
EPREHHIGLFPEDNGISFDTYSSSEHKEBALTHTQGRAVISDEAETSILNLSSIQT
ECSLDTVTSEQCYAAFRKIGLDYGEGYQGIEKVVVGKDQLLAKISLEAFLKNDKQHFA
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SKALEGTGISLTNDEGLGLDQIISBRQRAVLPRAVPDTNVWREDKLAMPSLLAMPALA
SWALEGTGTSTRULFETYPUMIYTLFSDELKIAAEPEPPFGEYGIDSIILAQUVG
QMNQQINGDIDPSIILEEYPTIESFAHWLISKVDISRVLAPSYVEKQPSAKQK
LVPFQNPQQISHEKTALLAEDIAIGLGCKRPGAFTLEEFTLEFFYPTER
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CAEGIASLIKVALMIKHRQLVPFLSGNENMPYFDIEKTDLYFSRSQAEWKETTPAAAI
NCFADGGTNAHLIIEGWRDSAERPIRKKPLPLPELNRQPVLIKPSAQNVQKKVHSDTG
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GVILGEGVGWVLVKTVNQAVEDGDSIYAVIKAAAINNDGRTAGFSSPHLEAQKDVMLS
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similar to polyketide synthases
Gene 130 (1), 65-71 (1993)
93345824
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/transl_table=11
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RBS

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Submitted (10-JUL-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 127447)
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Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Mar 24, 1999 this sequence version replaced gi:4139379.
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                  PVTOHEAVQPAHASIHGLAGTMAKEYPHWKIRLLDLEKGCTWPVHIMFALLPANALGAWAYANGOWHOOQLIPYRSSLSGDTLYRKGGYYVYIGGAGYICEAWSEYMIRFALPANGANUWAYRNOOWHOOQLIPYRSSLSGDTLYRKGGYYVYIGGAGYICEAWSEYMIRFYOAQIV WIGRSQLNAAIOSKIDRLSALGPEPFYIAADAADKHSLQOAYEOYKKRHPHHHGIVHS AMVLEEQSLEKKKPEEFFAGLAAKIDYSIRMAQVERQBNVDFVLFFSSLVAHIKNYKQ SHYASGCTFAAAFADAFAHQISGSRACPVKVMNMCYWGNSEAAEDEHYVQLMNQIGLGLIEP AEAMKALEALLSGPYSQTAFIHTTRPVAVEGVNQNEF" 1670 c 1949 g 1903 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC006344 127447 bp DNA PRI 21-DEC-1999
Homo sapiens PAC clone RP4-726N20 from 7q32-q34, complete sequence.
AC006344
                      SKAENKVRKYDIDLCDENGRYCVRMGGASMRALDGEGHSKPQLLTDSQLTGHTVMIPV
WEPVSIJEAEDNASFAGKRAVLCGAAEADRTFIKHYPQISFVDIRPADDIEAIADKLO
AYGSIDHVLMIAPSHRGSIGSDGQEEAVLHLFKLVKACLQLGYGEKQLEWSLVTVQAQ
LHPSLMDSAFHATVGFIVSSVNAAGQAQTLSLPFALQEVDIFSPCPEKIWSYIRYSSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria: Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cordes, M., Wohldman, P., Pape, K. and Hotic, M. The sequence of Homo sapiens PAC clone RP4-726N20 Unpublished
                                                                                                                                                                                                                                                                                                                                                        7650 CACTGCTTTCTGGGCCAGTCAGCCAAACAGCTTTCATTC 7688
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Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
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Waterston, R.H.
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Direct Submission
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Direct Submission
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08-881509-10 x BSPOLKET
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LOCUS AC006344 1:
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Center: Washington University Genome Sequencing Center
                          Center code: WúGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@vatson.wustl.edu
Contact: Summary Statistics
                                                                                                                                        Center project name: H_DJ0726N20
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by This sequence was finished as follows unless otherwise noted: restriction digest.

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information http://www.nhgrlin.nh.gov/DIR/GTB/CHR7, send http://www.nhgri.nih.gov/DIR/GTB/CHR7 , send mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc MAPPING INFORMATION:

This clone was derived from human PAC library RPCI-4, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by Ioannou et al., Nature Genetics 6:84-9 (1994). The library is from SOURCE INFORMATION: one male donor.

The clone may be obtained either from Genome Systems, Inc. (http://www.genomesystems.com) or Research Genetics, Inc. (http://www.resgen.com); or from Pieter de Jong.

VECTOR: pCYPAC2 NEIGHBORING SEQUENCE INFORMATION: The clone sequenced to the left is RP4-529P3. Actual start of this clone is at base position 1 of RP4-726N20; actual end is at 127447

The run of A's from 48936 to 48936 may contain one less A, no read

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repeat_region

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Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                 Center project name: 18221
Center clone name: 695_J_20
Center clone name: 695_J_20
Center clone name; 695_J_20
Center clone name; 695_J_20
Center clone name; 695_J_20
Sequencing vector: M13, M79815; 100% of reads
Chemistry: Dye-terminator B19 Dye; 100% of reads
Assembly program: Phrap: version 0.960731
Consensus quality: 145191 bases at least 040
Consensus quality: 148687 bases at least 020
Insert size: 150000; agarose-fp
Insert size: 151312; sum-of-contigs
Quality coverage: 4.4 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32233; gap of 100 bp. 100 bp. 40916; contig of 8683 bp in length 41016; gap of 100 bp. 50385; contig of 9369 bp in length 50485; gap of 100 bp. 11240 bp in length 6885; man of 100 bp. 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102408 102507; gap of 100 bp 102508 152512; contig of 50005 bp in length.
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82957 102407: contig of 19451 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9583: gap of 100 bp 15910: contig of 6327 bp in length 16010: gap of 100 bp 22585: gap of 100 bp 22585: gap of 100 bp 2333: contig of 9548 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
f 3233 bp in length
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of 3365 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1644: contig of 1644 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1645 1744: gap of 100 bp
1745, 2685: contig of 941 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="RP11-695J20"
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                                                                                        Web site: http://www-seg.wi.mit.edu
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6018: contig of
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.----- Genome Center
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82856: cont
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                                                              Center code: WIBR
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9484 9583:
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• All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AC025799 152512 bp DNA AC025799 15. WORKING DRAFT
DEFINITION Homo sapiens chromosome 15 clone RP11-695JZ0 map 15, WORKING DRAFT
SEQUENCE, 13 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152512)
                                                                                                                                                                           7523. .7578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AC006344 from: 1 to: 127447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 15, clone RP11-695J20 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TyrCysLeuValGlyArgSerAlaArgGlnLeuThr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
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7523. 7578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 152512)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC025799.2 GI:7387408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity: 91.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
08-881509-10 x AC006344/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
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                          repeat_region
                                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                            misc_feature
                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
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ORGANISM

REFERENCE AUTHORS

ACCESSION VERSION KEYWORDS JOURNAL REFERENCE

TITLE

AUTHORS

JOURNAL

COMMENT

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TITLE
JOURNAL
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Anderson, S., Baldwin, J., Bada, N., Bada, F., Boyslavkiy, L., Banderson, S., Baldwin, J., Barna, N., Bada, F., Boyslavkiy, L., Boukhalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Dodge, S., Domino, M., Doyle, M., Fenestor, J., Gardyna, S., Ginde, S., Goytte, M., Garlam, L., Hondon, J., Gardyna, S., Ginde, S., Goytte, M., Graham, L., Hoxland, J.C., Illev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Largocque, K., Lehcozky, J., Levinde, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McTuw, J., Mache, D., McCurk, A., McKernan, K., McPheeters, R., Meldrim, J., Mardus, L., Mihova, T., Miranda, C., Mlengan, V., Raymond, C., Nenn, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, C., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vashliev, H., Viel, R., Vo, A., Wilson, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AC023303 169181 bp DNA HTG 26-MAY-2000
DEFINITION Homo sapiens clone RP11-28L11, WORKING DRAFT SEQUENCE, 26 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 169181)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1201 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 81.818
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a 26845 c 27061 g 48178 t
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                                                                                                              .40916
                                                                                                                                                                  41017. .50385
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81.818
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08-881509-10 x AC025799/rev
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     misc_feature
                                                       misc_feature
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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
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Submitted (11-FEB-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 25, 2000 this sequence version replaced gi:7139695. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                         Center: Whitehead Institute/ MIT Center for Genome Research
Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequencing vector: M13, M77815; 100% of reads Sequencing vector: M13, M77815; 100% of reads Chemistry: Dye-terninator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 156445 bases at least Q40 Consensus quality: 163125 bases at least Q30 Consensus quality: 16395 bases at least Q20 Insert size: 173000; agarose-fp Insert size: 173000; agarose-fp Insert size: 166681; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality coverage: 4.6 in 020 bases; agarose-fp Quality coverage: 4.8 in 020 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site: http://www.seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Center`project Information
Center`project name: L4778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7119: gap of 100 bp in length 2831: contig of 100 bp in length 2831: contig of 1547 bp in length 100 bp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 1746: cont.y ... 100 bp
1747 1846: gap of 100 bp
1847 3452: contig of 1606 bp in length
3453 3552: gap of 100 bp
17453 3552: gap of 1714 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp
f 1653 bp in length
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18041 21065: cont1g of 3025 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 contig of 2409 bp in length
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43197: contig of 4993 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p of 100 bp
contig of 4873 bp in length
p of 100 bp
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7019: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center clone name: 28_L_11
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53635: con+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32507:
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15431: cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15432 15531; gap of
15532 17940; cont
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Center code: WIBR
                                                                           Direct Submission
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8312 98
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27424 27523:
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43298 481
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32508 32607;
32608 381
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117574 117673: gap of 100 bp 117574 117673: gap of 100 bp 117674 136527: contig of 18884 bp in length 136528 136627: gap of 100 bp 136628 169181: contig of 32554 bp in length. Location/Qualifiers
                                                                                                76616 76715: gap of 100 bp
76716 86772: contig of 10057 bp in length
86773 86872: gap of 100 bp
86873 99484: contig of 12612 bp in length
                                                                                                                                                                          99485 99584: gap of 100 bp
99585 117573: contig of 17989 bp in length
  60402 64778: contig of 4377 bp in length 64779 64878: gap of 100 bp 64879 69685: contig of 4807 bp in length
                                                             69686 69785: gap of 100 bp | 109786 76615: contig of 6830 bp in length
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64879. .69685
/note="assembly_fragment
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/note="assembly_fragment"
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1312. .9858
note="assembly_fragment"
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'note="assembly_fragment"
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'note="assembly_fragment"
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/note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vector_side:left"
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Direct Submission
Submitted (12-SEP-1997) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
3 (bases 1 to 188741)
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Submitted (03-FEB-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
4 (bases 1 to 188741)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-FEB-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukāryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Primates, Catarrhini; Hominidae, Homo.
1 (bases 1 to 188741)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
Locus Ac002542 108741 bp DNA PRI 04-FE
DEFINITION Human BAC clone CTB-114A6 from 7q31, complete sequence.
ACCESSION AC002542
                                                                                         2507 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Davidson, S., Rohlfing, T., David, M. and Ahrens, C. The sequence of H. sapiens BAC clone CTB-114A6 Unpublished
                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AC023303 from: 1 to: 169181
                                                                                                                                                                                                                                                            Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40492 TACTGCTTAGTGGGTAGAAGTTCAAGTAAGTTGTCA 40457
                 ture 136628. 169181

A6277 a 39522 c 38462 g 42413 t
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                                                                                                                                                                                                                 Length:
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117674. .136527
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Waterston, R.
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4.091<sup>-</sup>
91.667
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08-881509-10 x AC023303/rev
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       misc_feature
                                                        misc_feature
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                                                                                                   BASE COUNT
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JOURNAL
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repeat_region
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             The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University, and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DIR/GTB/CHR7 or send
                                                                                                                                                                                                                                                                                                                                                                                                     NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is RP5-866N18. The actual start of
this clone is at base position 1 of CTB-114A6; actual end is at
188741 of CTB-114A6. This clone is part of an unanchored island,
                                                                                                                                                                                                                                This clone is from the first release of the human BAC library. The library contains cloned DNA from a human male fibroblast cell line 9785K. See: Shizuya et al., Proc. Natl. Acad. Sci. USA 89:8794-7 (1992); Kim et al., Genomics 34:213-8 (1996). The clone is available from Research Genetics, Inc. (http://www.resgen.com).
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12714. 13075
/note="match to EST AA082591 (NID:g1624650) zn23h10.rl"
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/rpt_family="L1"
2834. .3145
/note="match to EST H65143 (NID:g1023883) yu64c07.rl"
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/clone_lib="CITB-978SK-B"
/map="7q31"
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complement(19061, 19320 /rpt_family="ALU"
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/db_xref="taxon:9606"
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/rpt_family="ALU"
complement(11229. .11249)
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3942. //r
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12385. .12720
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14499. 14700
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14873 14945
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/rpt_family="ALU"
20495. .20538
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11804. .12114
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /chromosome="7"
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MAPPING INFORMATION:
                                                                                                                                                                                                             SOURCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                pBeloBAC11
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25029. .2523
/note="match to EST N78558 (NID:91241259) yz79908.rl"
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/rpp_family="11"
3664. 36946
/note="match to EST R07221 (NID:9759144) yf14b06.rl"
36664. 37002
/note="match to EST_R07091 (NID:9759014) yf13f06.rl"
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/note="match to EST R07169 (NID:9759092) yf14b06.sl"
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complement(28075. .28106)
/rpt_family="L1"
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complement(30271. .30330)
/rpt_family="L1"
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complement(30633. 31188)
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complement(41783. .41819)
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24574. 24865
/rpt_family="L1"
complement(20938.
/rpt_family="L1"
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86219. .36244
                                                         'rpt_family="L1"
3539. .23838
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complement(34401.
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complement(41704.
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34254. 34376
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56782. .56850
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56166. .56187
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                                            .23198
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/rpt_family="L1"

08-881509-10.rge

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                                                                                       FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                \frac{\text{BCUBO}\overline{0}10}{\text{Sacillus subtilis complete genome (section 10 of 21): from 1781201}}
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Submifted (18-NOV-1997) I. Moszer, A. Danchin, Institut Pasteur,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The complete genome sequence of the gram-positive bacterium Bacillus subtilis
Nature 390 (6657), 249-256 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Yoshida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, H. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                              Length: 12
Gaps: 0
Percent Identity: 66.667
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                                                                                                                          /gene="WUGSC:H_RG114A06.1"
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                       /rpt_family="ALU"
59637. .59927
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299113 AL009126
299113.1 GI:2634090
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Percent Similarity: 91.667
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08-881509-10 x AC002542
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Locus BSUB0010 2
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/translation="NNEDLYPMFSGGGSQYYHMGKELFKENTVFRQSMLEMDAIAARR IGTSIVEETYHPGKRVSDPFDSILFSHPATEMIEYSLYKVLEDRGIYPDYJVGSVWEN SCOKGKMLATILDRPQLINDHPQLFGNSELISINYDSHFVISGEEDHIRKIMEDLKEKG ILCOLLEPVSYAFHSELIDPAESAYABFLRSKRFQKRSIPIVSSLTGSCLHVMDENFFW NAVRROMMFREAIRYLESQHTCKFIDLGPSGTLAAFVKQLIPGDSADRCCSIITPFHQ
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Enpysnlnktqetqpalyvvnalsylkkirdeeyvaralkeshelgeynalfaaeafdf
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Sgkkdeiekaaslfetmtevtmvlplnvsgafhskymnakrefeberhafyfsppsi
PVISNVYAKPYTYEFWKQTLADQINHSVKMTDSISYLMKKGHMEFEEVGPGNVLTGLI
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DDHQTISIGNTRAQCLLTPGHTAGGMCYLFSESIFTGDTVFTEGCGICEDDGSSAEEM
FDSIQRIKSEVSPHVRVYPGHSFGKSPGHSIKDLYQHNIYFQIDKKEYFFKFRTRKNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ALRHYFSTQDELLAFAMKIVQEKVTDRIKDIAVRDLDFKEKTQILLEMVPTNEETIR
EMEVWFAFTAXARHKKDMFDASHDGIFSGMRNLIAYLDESDLLKQNADKDIEABRLYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MPKQIDHEKRRKQIAEATWRVILERGMEGASARNIAKEAGLSLG
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Regulation de l'Expression Genetique, 28 rue du Docteur Roux, 75724
                           Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr, adanchin@pasteur.fr Phone: +33 (0)1 45 68 84 41, Fax: +33 (0)1 45
                                                                                                                                                                                                                                                                                                                                    /function="regulation of the polyketide synthase operon
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                                                                                                                                                               /organism="Bacillus subtilis"
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                                                                                                              Location/Qualifiers
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/transl_table=11
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/transl_table=11
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/gene="pksc"
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gene

CDS

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/product="cytochrome P450 hydroxylase PikC"
/protein_id="AAC68886.1"
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                                                                                                                                                                                          Quality: 45.00 Length: 13
Ratio: 3.462 Gaps 6 Gaps 0
Percent Similarity: 100.000 Percent Identity: 53.846
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/strain="AFTCC15439"
/db xref="taxon:54571"
/db_xref="ATCC:15439"
                                                                                                                                                                                                                                                                                                                                                                                                                                       44804 CACTGCTTTCTGGGCCAGTCAACCAAACAGCTTTCATTC 44842
                                                                                                                                                                                                                                                                                                                                                                                                        1 TyrCysLeuValGlyArgSerAlaArgGlnLeuThrPhe 13
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122. .1372
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                                                                                                                                                                                                                                                                              alignment_block: 08-881509-10 x BSUB0010
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                                                                                                                                                                                        Quality:
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ISRPEVAESFLSPAPENMIQKLLGENTTMNRAGTANDICVENSLIAK
ISRPEVAESFLSPAPENMIQKLLGENTTMNRAGTANDICVENSLIAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VAYSLMPAMTSLRDEMMKKYOYRKKIRVGAAGGIGTPEAAMAAFMLGADFILTGSINO
CTVEAATSDKVKDLLQOMNVQDTAYAPAGDMFESGSKVQVLKKGVFFPARANKLYELY
ORYGSIRELDAKMLAQLEEKYFKRSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Translation-"MTKCNLPEVVYTCYGOTASIGGGKEDFASSLLSGRHAFDVMKRS
GRQKDSRFIGAEIASLSYPDRLSKKMLRKASFSSRAALVTLTEAWEEAELDDADSSRI
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SITGHGLASAAGIVEILIGYLLQWKKSALHPSRNLDHPIDDSFHWVNEKSISYRIKNALS
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IENHLDRRYQLSWBEVELLFKGSGWVRFGTRNVKLDFEMIPGIMGSTQERFFLEEI
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                                                                                                                    function="involved in polyketide synthesis"
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SLKNLNTVEYFRTPERKFTR"
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6780. .8030
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'gene="pksE"
                                                                           1189. .6141
/gene="pksE"
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9280. 10059
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HYWTLMTKPISVQEASEWGLIDAFDAESDVLLRKHLLRLRRLNKKGIAHYKQFMSSLD
HQVSRAKATALTANQDMFSDPQNQMGIIRYVETGQFPWEDQ"
10099-101848
10099. .10848
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Hydroxylation of macrolactones YC-17 and narbomycin is mediated by
Hydroxylation of cytochrome P450 in Streptomyces venezuelae
Chem. Biol. 5 (11), 661-667 (1998)
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
1 (bases 1 to 4342)
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Direct Submission
Submitted (17-JUL-1998) Department of Microbiology, University,
420 Delaware Street SE 1060, P.O. Box 196, Minneapolis, MN 55455,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Xue,Y., Zhao,L., Liu,H.w. and Sherman,D.H.
A gene cluster for macrolide antibiotic biosynthesis in streptomyces venezuelae: architecture of metabolic diversity Proc. Natl. Acad. Sci. U.S.A. 95 (21), 12111-12116 (1998)
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Streptomyces venezuelae pikCD operon, complete sequence.
AF079139
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AL1391061 Homo sapiens chr
AL139383 Homo sapiens chr
AP002866 Oryza sativa gen
AC025318 Homo sapiens chr
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YYCLVGGSARQLIFGSGTQLTVLPDIONPDPAVYQLROSKSSDKSYCLFTDEPSGTAV
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55. 801
365 c 294 g 351 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J gene; junction; T cell receptor; TCR junctional sequence; V gene.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.

(Dases 1 to 1318)
Jantzer, P.U. and Schendel, D.J.
Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carchnomas express T cell receptors characteristic of a Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-JAN-1997
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H.sapiens mRNA for rearranged TCR junctional sequences.
X98410
                                                155632
163066
166753
167277
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1. .804
/note="unnamed protein product"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
Location/Qualifiers
                                                                       5.8e+03
5.9e+03
6.0e+03
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                                                                                                                                                                                                                                               A93127 1341 bp DNA Sequence 1 from Patent EP0816496. A93127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="unidentified"
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unclassified.
1 (bases 1 to 1341)
Schendel, D.J.
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gb_pl2:AP002866
gb_htg11:AC025318
                                       gb_htg22:AL391061
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CDS
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BASE COUNT 3
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186787 | ACO73557 Homo sapiens chromd
195761 | ACO18895 Homo sapiens chromd
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Database sequences: 1118133
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Query: 08-881509-1
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gb_htg6:ACO16721
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                                                      Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology, Goethestr. 31, D- 80336 Munich, FRG Location/Qualifiers
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/protein_id="CAA67057.1"
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T.-Cells specific for kidney carcinoma Patent: EP 0816496-A 07-JAN-1998;
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/db_xref="taxon:9606"
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Jantzer, P.
Direct Submission
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 39)
                                                                                                                                                                                                                                                                               HSU30428 39 bp mRNA pri 01-AUG-1995
Human isolate M74.T-ceIl receptor alpha V-J junction (TCR Valpha
3/J alpha 22) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product==T-cell receptor alpha V-J junction"
/protein_id="AAA73607.1"
/db_xref="GI:915482"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 69:231
                                  Percent Identity: 83.333
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                                                                                                                                                                                                    Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                              2 CysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
Length:
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/isolate="M74"
                                                                                                                                     Align seg 1/1 to: A93139 from: 1 to: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="blood"
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92.308
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                                                                                                     08^{-}88150\overline{9}-1 \times A93133
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seq_name: gb_pr7:HSU30448

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AUTHORS
                                   JOURNAL.
                                                   REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AC021965 186797 bp DNA HTG 04-APR-2000
DEFINITION HOMO Sapiens clone RP11-47505, WORKING DRAFT SEQUENCE, 11 unordered
                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhin; Hominidae; Homo.

1 (bases 1 to 39)

Dave, V. P., Larche, M., Rencher, S. D., Koop, B. F. and Hurwitz, J. L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation

Hum. Immunol. 37 (3), 178-184 (1993)
                               HSU30148 39 bp mRNA PRI 01-AUG-1995
Human isolate M94 T-cell receptor alpha V-J junction (TCR Valpha
3/J alpha 22) mRNA, partial cds.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 186797)
                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="T-cell receptor alpha V-J junction"
/protein_id="AAA73621.1"
/db_xref="G1:915516"
/translation="FCVSSGSARQLTF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /isolate="M94"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC021965
AC021965.3 GI:7408035
HTG: HTGS_PHASE1; HTGS_DRAFT.
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Direct Submission
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             seq_documentation_block:
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                                                                                                                                                             Homo saptens
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08-881509-1 x HSU30448
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TITLE
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A (dases I to 180/y),

Birran, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,

Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Bedda, F.,

Boguslavkly, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, A.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,

Perrelra, P., Fitzhugh, W., Forrest, C., Gage, D., Galagan, J.,

Gardyna, S., Grant, G., Hagos, B., Haeford, A., Horton, L.,

Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,

Macdonald, P., Marquis, N., McEwan, P., McClork, K.,

McMeners, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,

McMoheeters, R., Meldrim, J., Mereus, L., Morrow, J., Naylor, J.,

Norman, C. H., O'Connor, T., O'Donnell, P., Olivar, T. M., Peterson, K.,

Pierrell, A., Vasail, G., Pollara, Y., Raymond, C., Riley, R., Rothman, D.,

Stojanovic, N., Subramanian, A., Talamas, J., Tesieve, S., Theodore, J.,

Inrell, A., Wassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. J.,

Zimmer, A. and Zody, M.

Submitted (12-7Nn-200) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

All repeats were identified using Repeatmasker: html

Center: Whitehead Institute/ MIT Centem for Genome Center: Whitehead Institute/ MIT Centem for Genome Center: Whitehead Institute/ MIT Center for Genome Center: Whitehead Institute/ MIT Center for Genome Center.

Center: Whitehead Institute/ MIT Center for Genome Center.
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* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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20838: contig of 5269 bp in length
Birren, B., Linton, L., Nusbaum, C. and Lander, E. Homo sapiens, clone RP11-47555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ter project Information ter project name: L6069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: 475_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center project name:
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                                                                          Unpublished
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/Lranslation-"MRQVARVIVFLTLSTLSLAKTTQPISMDSYEGGEVNITCNHNDI
ATSDYIMWYQQFPNQGPRFIIQGYKANIANEVASLFIPTDRKSSTLSLPRVALSDTAV
YYCLVGDRYSGGSANRLJFGKGTHLIVQPYIQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alpha (TCE A) mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vertebrata; Euteleostomi;
2 (bases 1 to 506)
Coh,T.K. and Hyde,K.D.
Direct Submission
Submitted (28-JUN-1999), Ecology & Biodiversity, The University of
Hong Kong, Pokfulam Road, Hong Kong SAR, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-JAN-1995
                                                                                                                                                                                  /product="internal transcribed spacer 1"
183. .339
                                                                                                                                                                                                                                                                       /product="internal transcribed;spacer 2'
                                                                                                              /organism="Drechslera tritici-repentis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca mulatta (clone MMVA165) T-cell receptor
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/protein_id="AAA60416.1"
/db_xref="GI:623133"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Mammalia; Eutheria; Primates; Catarrhini
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                                                                                                                                                                                               Percent Identity:
                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                         Gaps:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AF163060 from. 1 to: 506
                                                                                                                                                /db_xref="taxon:132100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90 TGTTTACTTGGCGGGTCCGCCCCCCAATG 119
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/clone="MWVA165"
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                                                                                     Location/Qualifiers
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1 (bases 1 to 402)
                                                                                                                                 /strain="7819-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                            340. .506 ./note="ITS2"
                                                                                                                                                                                /note="ITS1"
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Percent Similarity: 100.000
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L38878
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LOCUS MACTCRAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drechslera tritici-repentis.

Drechslera tritici-repentis

Enkaryota; Fungi; Ascomycota; Pleosporales; Pleosporaceae;
anamorphic Pleosporaceae; Drechslera.

1 (bases 1 to 500)

Goh, T. K. and Hyde, K. D.
Generic separation in the Helminthosporium-complex, based on sequence analysis of the rDNA
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               118262 118361: gap of 100 bp
118362 148993: contig of 30632 bp in length
148994 149093: gap of 100 bp
149094 186797: contig of 37704 bp in length.
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                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="RP11-47515"
/clone_lib="RPCI-11 Human Male BAC"
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1 33479 c 31559 g 61128 t
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/note="assembly_fragment"
5390. .11030
/note="assembly_fragment"
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note="assembly_fragment"
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149094. .186797
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84.615
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LOCUS AF163060
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Nopptera; Endopterygota; Nopptera; Nematocera; Culicoidae; Culicidae; Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web : www.genoscope.cns.fr) 2 (bases 1 to 995) 8Cth.C.W. Brey.P.T. Ke,Z., Collins,F.H. and Weissenbach,J. Direct Submission
                                                                                                                                                                                                                                                       1 TyrCysLeuVal......GlyGlySerAlaArgGlnLeuTh 12
                                                                                                                 Percent Identity: 61.111
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722 c 216 g 269 t
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/clone="09C07"
/clone_lib="NotreDame1"
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                                                                                            3.654
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92.308
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08-881509-1 x CNS01HNL/rev
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08-881509-1 x MACTCRAAT
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                                                                                                   Percent Similarity:
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Ratio:
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seq_documentation_block:
LOCUS ACO16721 185286 bp DNA HTG 07-JUL-2000
DEFINITION Homo sapiens chromosome 2 clone RP11-327J6, WORKING DRAFT SEQUENCE,
ACCESSION AC016721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammallai; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 185286) Waterston, R. H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             * NOTE: This is a 'working draft' sequence. It currently consists of 19 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MO 63108, USA
On Mar 13, 2000 this sequence version replaced g1:7022633
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Center code: WUGSC
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The state of the sta
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contig of 6653 bp in length
gap of unknown length
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gap of unknown length
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                                                          718 TATTGCCTTATAGGACACAAGGCCCGCAAGCTTAATTTT 680
1 TyrCysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence of Homo sapiens clone Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of 5997
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gap of unknown
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18480:
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                                                                                                                                                                                          seq_name: gb_htg6:AC016721
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1825 others
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contig of 12388 bp in length
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                                                                                                                                                        unknown length
of 13818 bp in length
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of 11806 bp in length
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                              gap of unknown length
contig of 9375 bp in length
gap of unknown length
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contig of 7224 bp in length gap of unknown length contig of 6911 bp in length
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rature 122011. 134398
eature 70ce="assembly_name:Contig21"
rature 134499. 158377
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reature 158478. 185286
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seature 158478. 185286
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/note="assembly_name:Contig23"
                                                                                                                    unknown length
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/note="assembly_name:Contig17"
78728. .92545
/note="assembly_name:Contig18"
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/note="assembly_name:Contig15"
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                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
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13

Length:

Quality: 47.00

alignment_scores:

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GE 2 (bases 1 to 186/8/)

RS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Beda, F., Boduslavkiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Campoplano, A., Cooke, P., DeAellano, K., Dewar, K., Diaz, J.S., Collymore, A., Cooke, P., DeAellano, K., Dewar, K., Diaz, J.S., Galageno, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Gage, D., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Katatas, A., Klein, J., Lakoque, K., Lamazares, R., Landers, T., Leboczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPhenga, V., Morrow, J., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Peterson, T., O'Donnell, P., Wurphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Pisani, C., Pollara, V., Raymond, C., Riley, R., Regov, P., Rothman, D., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Volang, C., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Volang, C., Zainoun, J., Zimmer, A. and Zody, M., Trigilio, J., Volang, C., Zainoun, J., Zimmer, A. and Zody, M., Subramanian, A., Wassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Volang, C., Wassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Yong, Charles Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I, Oases; I to 186787)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.
HOMO. sapiens chromosome 2, clone RP11-70708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC073557 186787 bp DNA HTG 04-OCT-2000 HTG OACCT-2000 HOMO sapiens chromosome 2 clone RP11-70708 map 2, WORKING DRAFT SEQUENCE, 30 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center clone name: 707_08

Sequencing vector: M13, M78815; 100% of reads
Sequencing vector: M3, M78815; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality; 17265 bases at least Q30

Consensus quality: 179967 bases at least Q30

Consensus quality: 182697 bases at least Q20
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                                                                                                                                                                             Align seg 1/1 to reverse of: AC016721 from: 1 to; \mathring{1}85286
                    Percent Identity: 53.846
                                                                                                                                                                                                                                                                                               1 TyrCysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
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3.917
92.308
                                                                                                 alignment_block:
08-881509-1 x AC016721/rev
                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_htg17:AC073557
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LOCUS AC073557 18
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   Ratio:
Percent Similarity:
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KEYWORDS
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NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N. but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
Insert size: 192000; agarose-fp
Insert size: 183887; sum-of-contigs
Quality coverage: 4.2 in Q20 bases; agarose-fp
Quality coverage: 4.4 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78156 78255: gap of 100 bp 85418 contig of 7163 bp in length 85419 85518: gap of 100 bp 85419 85518: gap of 100 bp 85419 85518: gap of 100 bp 85519 92963: contig of 7164 bp in length 92963: gap of 100 bp 100677 100361: contig of 7644 bp in length 100677 100361: contig of 9588 bp in length 110362 120397: contig of 9388 bp in length 110462 120397: contig of 9143 bp in length 120398 120498: gap of 100 bp 120491 129540: contig of 9143 bp in length 129741 142134: contig of 1304 bp in length 142155 156210: contig of 13956 bp in length 142155 156210: contig of 13956 bp in length 142155 156210: contig of 13956 bp in length 142255 156210: contig of 13956 bp in length 142255 156210: contig of 13956 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3076 3175; gap of 100 bp 1375 434 4445 contig of 1169 bp in length 4445 5450; contig of 100 bp 100 b
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40126: conf
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43734 47149: conf
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60061: cont
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64006: cont
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1186787 /organism="Homo sapiens" /db_xref="taxon:9606" //dpromosome="2"	="RP11-70708" -"RP11-70708" 110="RPCI-11 Human 155===================================	nd:SP6 side:left 4344	മേവ	ass 665	a 83	assembly_ 32482	assembly_ .33676	assembly_ .34786	assembly_ .37514	ssembly_ 40126	"assembly_fragment" .43633	ssembly_ 47149	ssembly_ 51088	assembly_ .54290	assembly_ .60061	assembly_ .64006	ssembly_ 68134	ssembly_ 72939	ssembly_ 78155	ssembly_ 85418	assembly_fragment" .92962	assembly_fragment" .100676	assembly_fragment" .110361	assembly_fragment" .120397	ss.	ssemb.	.ssembly_fragment" .156210	SS.	ssembly_fragment.185820	ssembly_fragmen.186787		Length: Gaps:
/organ /db_xre /chromc	clone clone clone 30	1.67	ote=	ote=	te.	ote-	ote= 583.	В -	te. 87.	te= 15.	te- 27.	note= 3734.	. 0	90	å .:	90			te= 40.		٠.	ž.					/note="a 142255.	/note="a 156311.	Ŭ (i	/note="a 185921. /pote="a	ב ט ט	47.00 3.917
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DEFINITION

ACCESSION

VERSION KEYWORDS

ORGANISM

SOURCE

REFERENCE AUTHORS

JOURNAL

TITLE

COMMENT

AUTHORS

JOURNAL REFERENCE

TITLE

08-881509-1.rge

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contig of 11545 bp in length

gap of unknown length

contig of 16786 bp in length

gap of unknown length

contig of 14608 bp in length

gap of unknown length

contig of 22332 bp in length.
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gap of unknown length
contig of 8024 bp in length
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of 8509 bp in length
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4471. .6915
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14419. 17005
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/db_xref="taxon:9606"
/chromosome="5"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
On Aug 12, 2000 this sequence version replaced gi:7658490.
                                                                                                                                                                                                                   AC018895 195761 bp DNA HTG 12-AUG-2000
Homo sapiens chromosome 5 clone RP11-569B5, WORKING DRAFT SEQUENCE,
27 unordered pieces.
                                                                                                                                                                                                                                                                                                                        Eukaryota, metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 195761)
                                                                                                                                                                                                             12-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 27 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert size: 191000; agarose-fp
Insert size: 193161; sum-of-contigs
Quality coverage: 3.79 in Q20 bases; agarose-fp
Quality coverage: 3.78 in Q20 bases; sum-of-contigs
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gap of unknown length
contig of 2708 bp in length
gap of unknown length
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                                                                                                                            Percent Identity: 53.846
                                                                                                            1 TyrCysLeuValGlyGlySerAlaArgGlnLeuThrPhe 13
                                                                               Align seg 1/1 to: AC073557 from: 1 to: 186787
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HTG; HTGS_PHASE1; HTGS_DRAFT.
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Waterston, R.H.
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          Percent Similarity: 92.308
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                                                                                                                                                                         seq_name: gb_htg7:AC018895
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                                                      08-881509-1 \times AC073557
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vector_side:right"

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HSM800003 1492 bp mRNA PRI 18-FEB-2000
Homo sapiens mRNA; cDNA DKFZp56411916 (from clone DKFZp56411916).
AL049218
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Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by BMF2 (Biomedical Research Center at the Charite,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Koehrer, K., Beyer, A., Mewes, H.W., Gassenhuber, J. and Wiemann, S. Direct Submission
Submitted (10-MAR-1999) MIPS, Am Klopferspitz 18a, D-82152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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              /note="assembly_name:Contig21"
                                  44665. .50380
/note="assembly_name:Contig22"
                                                                       50481. 58039 /note="assembly_name:Contig23"
                                                                                                                             /note="assembly_name:Contig24"
                                                                                                                                                          ວ4ວວ3. ./ບລວ
/note="assembly_name:Contig25"
                                                                                                                                                                                  71094, 78868 - 70046-"assembly_name:Contig26" 78969, 85138 / 70ce-"assembly_name:Contig27
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/note="assembly_name:Contig29"
                                                                                                                                                                                                                                                                                                                                                                                   99595. .108103
/note="assembly_name:Contig30"
108204. .118247
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130191. 1141735
/note="assembly_name:Contig33"
141836. 158621
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                                                                                                                                                                                                                                                                                                      85239. . 93262
/note="assembly_name:Contig28"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig31"
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173430. .195761
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a 33956 c 35611.9 62640 t
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Percent Similarity: 84.615
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08-881509-1 x AC018895/rev
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LOCUS HSM800003
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ALECT SUMMISSION.

Submitted (19-JUL-2000) Sanger Centre, Hinxton, Cambridgeshire, CBLO 15A, UK. E-mail enquiries: hunquery@sanger.ac.uk Clone requests: clonerequestgeanger.ac.uk

On Jul 7, 2000 this sequence version replaced gi:7940159.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences with an all overlapping clone, as we submit sequences with conly a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the feature feature feature is an annotation using the 'unsure'
                                                            This clone (DKFZp56411916) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/.
Berlin/Germany) within the cDNA sequencing consortium of the German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSDJ22117 86654 bp DNA PRI 24-JUL-2000 Human DNA sequence from clone RPI-22117 on chromosome 6q11.1-12. Contains the 3' end of the gene KIAA0244, the 3' end of the gene for a novel protein with EGF-like and laminin G domains, ESTS, STSS and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 86654)
                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKRZp56411916"
/clone=lb="564 (synonym: hfbr2). Vector pAMP1; host
Xl-2blue; sites NotI + SalI"
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/tissue_type="brain"
1456. 1461
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AL050329.12 GI:8977876
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Percent Similarity: 91.667
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                                      Genome Project
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LOCUS HSDJ22117 {
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KEYWORDS
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FEATURES

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http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at
                                                                                                          http://www.sanger.ac.uk/HGP/Chr6
RP1-2217 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1145. .4266
note="LIMA8 repeat: matches 6146. .6284 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2294. 2744
Anote="nigger2a repeat: matches 1. .434 of consensus" 3264. 3407
Anote="72 copies 2 mer tt 57% conserved"
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note="MLT2FB repeat: matches 367. .405 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5681. .6116
/note="LTR40b repeat: matches 25. .459 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1598. .4822
/note="MER46A repeat: matches 1. .236 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    463. .5571
/note="L2 repeat: matches 2587. .2692 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="AluJb repeat: matches 113. .197 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     312. .946
/note="FLAM_C repeat: matches 1. .133 of consensus"
complement(1059. .1556)
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note="MLT2FB repeat: matches 4. .365 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .798 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="MER1B repeat: matches 1. .337 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="AluSp repeat: matches 1. .288 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181. .516 'note="AluJb repeat: matches 1. .113 of consensus"
                                                                                                                                                                                                                              This sequence is the entire insert of clone RP1-22117. Location/Qualifiers
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/note="18 copies 2 mer gt 100% conserved"
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/note="HAL1 repeat: matches 458.
complement(1772. .2228)
/note="match: GSS: Em:A0772565"
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/note="match: GSS: Em:AQ883741"
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/note="match: GSS: Em:AQ677335"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="match: GSS: Em:AQ814479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1059. .1556)
/note="match: GSS: Em:AQ808506"
complement(1634. .2230)
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/note="match: GSS: Em:AQ321324"
1755. .2079
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on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="RPCI-1"
                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP1-22117"
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                                                                                                                                                                                                                                                                                                                                                       /chromosome="6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .380
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/gene="rdu/cil/.L"
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Em:AA218694 Em:AA329675 Em:AA789461 Em:AA13506
Em:AA2186 Em:AA329675 Em:AA789461 Em:AA23665
Em:AA680563 Em:AA32647 Em:AA186180 Em:C60394
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43212. _43356,43438. _43594,45339. _45455,47497. .47628,
48225. .48660,51018. .51213,51718. .51865,54146. .54235,
56162. .56357,56581. .60476)</pre>
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/note="LlMC/D repeat: matches 5728. .5868 of consensus"
13348. 13639
                                                                      12524. .12704
/note="L1MC5_repeat: matches 7510. .7707 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Alusc repeat: matches 51. .299 of consensus" 16995. .17140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="12 repeat: matches 2367. .2525 of consensus"
16745. .16994
                                                                                                                                                                                                                                                                                                                                           6995. 17140
note="AluSc repeat: matches 1. .146 of consensus"
                                                                                                                                                                                                                                          /note="AluJb repeat: matches 1. .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23421. .23451

/note="MIR repeat: matches 4. .34 of consensus"

23932. .24097

/note="MIR repeat: matches 88 . .261 of consensus"

24441. .24504

/note="32 coples 2 mer tt 71% conserved"

/note="32 coples 2 mer tt 71% conserved"

/note="32 coples 2 mer tt 71% conserved"

/note="32 coples 2 mer tt 71% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                         MADE1 repeat: matches 1. .79 of consensus".16635
                                                                                                                                                                                                                                                                                                                 /note="Alur repeat: matches 2. .311 of consensus"
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/product="dJ22117.1 (KIAA0244)"
25320. .25395
12333. .12747
/note="match: GSS: Em:AQ006173"
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Journal of this sequence of the control of the control of the sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the together with a note of the overlapping clone name. Note that the corresponding to the overlapping clone, as we submit sequences submission only a small overlap as described above. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known sequence is ambiguous, there is an annotation using the 'unsure'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL137881 143324 bp DNA PRI 29-JUN-2000
Human DNA sequence from clone RP11-40A8 on chromosome 13, complete
                                                                                                                                                                                                                                                                                                                                                                                                                           Joses. .33314

//Orde="Tandem repeat. Region contains single clone and forced join. Digest suggests there may be 200bp missing from the tandem repeat."
33331. .33623
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
/note="HAL1 repeat: matches 1551. .1627 of consensus" 25399. .25428
/note="15 copies 2 mer tt 90% conserved" 25782. .26672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-JUN-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clonerequests: clonerequest@sanger.ac.uk
                                                                                                  /note="HAL1 repeat: matches 147, .1094 of consensus"
                                                                                                                               28141. .28237
//ote="MER04 repeat: matches 2. .100 of consensus" 28930 .28930 .2895  
//note="25 copies 2 mer at 72% conserved" 32137 .32419
//note="Allos repeat: matches 1. .282 of consensus" //note="Allos repeat: matches 1. .282 of consensus"
                                                                                                                                                                                                                                                                                                                           note="AluY repeat: matches 83, .296 of consensus"
                                                                                                                                                                                                                                                                                                                                                                            'note="54 copies 2 mer cc 75% conserved"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 100.000 Percent Identity: 58.333
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08-881509-1 x HSDJ22I17
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LOCUS AL137881 1
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The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:
Em:, EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORNPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human

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This sequence is the entire insert of clone RP11-40A8 The true left end of clone RP11-547C18 is at 69479 in this sequence. The true right end of clone RP11-233H19 is at 14112 in this sequence.
chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at http://www.sanger.ac.uh/HCP/Chr13
RP11-40A8 is from the library RCI-11.1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                    19526. 19591
//note="Single clone region. Region contains reads from clone pcr only (oligos 162). Assembly is consistent with restriction digest."
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91.667 Percent Identity: 66.667
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                                                                                                                                                                                                                                                                                1. 143324
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/clone="RP11-40A8"
/clone_lib="RPCI-11.1"
19526. 19591
                                                                                                                                                                                                                                                             Location/Qualifiers
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Ratio:
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i AF127771 Homo sapiens cell-
i X66604 Pseudomonas sp. plas
i AE000662 Homo sapiens T-ce
i M94081 Human Tcr-C-delta g
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Jantzer, P.U. and Schendel, D.J.
Tumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of a secondary immune response.
                                                                                                                                                                                22-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JAN-1997
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Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission Submission Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology, Goethestr. 31, D- 80336 Munich, FRG Locátion/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             H.sapiens mRNA for rearranged TCR junctional sequences.
X98410
                           4091 1
8280 1
71153
97630
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                    unidentified
unclassified.
1 (bases 1 to 39)
Schendel,D.J.
T-cells specific for kidney carcinome
Patent: EP 0016496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH. (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="CAB69531.1"
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                         70.53
145.83
1.3e+03
1.9e+03
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/organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                          A93131 39 bp DNA
Sequence 5 from Patent EP0816496.
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                       126.30
120.64
103.36
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                       45.00
45.00
45.00
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Percent Similarity: 100.000
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LOCUS
                                                                                                                   seq_name: gb_pat1:A93131
                                                                                                                                                                                                                                                                    unidentified
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LOCUS
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                     gb_pr3:AF127771
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                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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gb_htg11:AC025530
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gb_pat1:A93127
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gb_pr8:HUMTCAZA
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gb_htg16:AC069255
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9b_pr8:HUMTCRACG
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                                                                                                                                                                                                                                                                        TGSARQITFGXCLVGGDTDKLIFGXCLVLSGSGRQITFGXCLVLSGSGRQLFFGXCLV
VSGSARQITFGXCLALGGSARQITFGXCLALAGSARQITFGXCLAPSGSARQITFGXC
LVAGGGNTPLVFGXCLVGSARQITFGXCLVGSARQITFGXXCLVGRSARQITFGXCL
ATGSARQITFGXCLVGAGGYQKVTFGXCLVLSGSARQITFGXCLVAFGXCLVGRSARQITFGX
CLVVLGGSQGNLIFGXCLVGPNNAGNULTFGXCLVATNQGRNCSDLW"
329 c 352 g 344 t 87 others
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LVSGSARQLTFGXCLDSGSARQLTFGXCLDSGSARQLTFGXCLPSGSARQLTFGXCLA
                                                                                                                                                                                                                 /translation="CLVGGSARQLTFGXCLATGSARQLTFGXCLVLSGSARQLTFGXC
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Homo sapiens mRNA for T cell receptor alpha chain V-J junctional
region (TCRAV7AJ16S3).
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T cell receptor; T cell receptor alpha chain; variable region
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Misko,I.S., Cross,S.M., Khanna,R., Elliott,S.L., Schmidt,C.,
Pye,S.J. and Silins,S.L.
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/protein_id="CAA67057.1"
/db_xref="G1:1770561"
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                                                                                                                /note="V gene/J gene junction"
/codon_start=1
                            /isolate="patients 22 and 26"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
             /organism-"Homo sapiens"
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Direct Submission
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Maggi, E. and Romagnani, 8.
Molecular basis of cross-reactivity among allergen-specific human T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS S69140 98 bp mRNA PRI 23-SEP-1994
DEFINITION TCR V alpha=T-cell receptor alpha-chain (allergen-specific) [human, grass sensitive individual VI 19, peripheral blood, mRNA Partial,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="This sequence comes from Fig. 3b; Protein sequence is in conflict with the conceptual translation"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo:
1 (bases 1 to 98)
Mohapatra, S.S., Mohapatra, S., Yang, M., Ansari, A.A., Parronchi, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells: T-cell receptor V alpha gene usage and epitope structure
Immunology 81 (1), 15-20 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genbank staff at the National Library of Medicine created this entry [NCBI gibbsq 144562] from the original journal article. This sequence comes from Fig. 3a. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /exception="Protein longer than coding region shown;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="DSATYFCAALPESARQLTFGSGTQLTVLPDION"
27 c 20 g 28 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        human peripheral blood grass-sensitive individual VI 19.
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/product="T-cell receptor alpha-chain"
/protein_id="AAB30244.1"
/db_xref="G1:545974"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="TcR V alpha"
/note="T-cell receptor alpha-chain"
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Percent Identity: 71.429
                                                                                                                                                  Length: 13
Gaps: 0
Percent Identity: 84.615
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/db_xref="taxon:9606"
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/cell_line="SP1"
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08-881509-2 x HSA235208
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T-cell receptor usage by anti-melanoma specific cytotoxic tumor-infiltrating lymphocytes. Detection of dominant tumor-specific T-cell clones by single strand conformational polymorphism and T-cell receptor

U Onpublished (1995)

E ( Loases I to 214)

E ( Loases I to 214)

E ( Loases I to 214)

Waitkus, R., Boyle, L.A., Hishii, M. and Andrews, D.M.

Direct Submission

Submitted (16-NOV-1995) James T. Kurnick, Pathology Research Laboratory, Massachusetts General Hospital, 149 East 13 St.,

Charlestown, MA 02129, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAA833012'1"
/db_xref="GI:1103937"
/translation="SIYSNGDKEDGRETAQLNKASQYVSLLIRDSQPSDSATYLCAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 87)
Yandevyver,C., Mertens,N., van den Elsen,P., Medaer,R., Raus,J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence
Eur. J. Immunol. 25 (4), 958-968 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HUMTCRACG 87 bp mRNA PRI 07-NOV-1995
Homo sapiens (clone NS1-F4) T cell receptor alpha chain (TCRA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clonal expansion of myelin basic protein-reactive T cells in
                        Waitkus, R., Boyle, L.A., Hishii, M. and Andrews, D.M.
                                                                                                                                                                                                                                                                                                                                                                                /cell_type="cytotoxic T-cell lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"T-cell receptor alpha chain"
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Gaps: 0
Percent Identity: 84.615
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L42801
L42801 GT:853662
T cell receptor alpha.
Homo sapiens (clone: NSI-F4) cDNA to mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="V alpha 2.1 J alpha 22
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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08-881509-2 x HSU40776
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YYCLVGGSARQLIFGSGTQLTVLPDIONPDPAVYQLRDSKSSDKSVCLFTDFDSQTNV
SQSKDSDVYITDKTVLDMRSMDFKSNSAVAMSNKSDFACANAFNNSIIPEDTFFPSPE
SSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLMSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MRQVARVIVFLTLSTLSLAKTTQPISMDSYEGQEVNITCSHNNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human T-cell receptor alpha chain (TCRAV2S1J22) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 214)
Kurnick,J.T., Ihara,A., Pervaiz,S., Pandolfi,F., Van,Den Elsen P.,
                                                                                                                                                                                                                                                                   22-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1995
                                                                                                                                                                                                                                                                PAT
                                                                                                      1 TyrCysLeuValLeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                               310 TACTGCCTCGTG...GGTGGTTCTGCAAGGCAACTGACCTTT 348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1341)
Schendel, D. J.
T-cells specific for kidney carcinome
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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/protein_id="CAB69529.1"
/db_xref="G1:6741517"
                                                                                                                                                                                                                                                     LOCUS A93127 1341 bp DNA
DEFINITION Sequence 1 from Patent EP0816496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="unidentified"
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                                                              to: S69140 from: 1 to: 98
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LOCUS A93127
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unclassified.
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08-881509-2 x A93127
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alignment_block:
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DEFINITION

ACCESSION

KEYWORDS

VERSION SOURCE ORGANISM

REFERENCE AUTHORS

source

FEATURES

ORGANISM

REFERENCE AUTHORS JOURNAL

TITLE

ACCESSION

VERSION

KEYWORDS

SOURCE

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                                                                                                                                                                                                                                                                                                                                                                                                              SOURCE
                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="metllevlsgtlimoltwvrsqopvqspqavilregedavincs
SSRALYSVHWYRQKHGEAPVFLMILLKGGEQRGHEKISASFNEKKQQSSLYLTASQLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCR V alpha =T cell receptor variable alpha chain [human, MT-ALL, Genomic Mutant, 716 nt].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="This sequence comes from Figure 4; conceptual translation presented here differs from translation in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 63879] from the original journal article. This sequence comes from Figure 4.
                                                              04-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="T cell receptor variable alpha chain"
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/db_xref="G1:853663"
/translation="YFCAEASGSARQIAFGSGTQLTVLPDIQK"
                                                                                                                                                                                                                                                                                                            Percent Identity: 71.429
                                                                                                                                                                                                                                                                                                                                                                                                                                             4 TITICIGCAGAGGCCTCTGGTTCTGCAAGGCAACTGACCTTT 45
                                                                                                                                                                                                                                                                                                                                                                                                                 1 TyrCysLeuValLeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Immunol. 147 (10), 3336-3341 (1991) 92043697
                                                                                                                                                                                                                                                                                                Gaps:
                                                                                                                                                                                                                                                                                Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .>716)
                                                                                                                             /db_xref="GDB:G00-120-404"
                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: HUMTCRACG from: 1 to: 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="TCR V&agr"
join(58. 109,340.
/gene="TCR V alpha"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="TCR V alpha"
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                                                                                                                                                                                                         21 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/clone="NS1-F4"
           /map="14q11.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      publication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          716 bp
                                            "TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S63879.1 GI:238692
                                                                                                                                                                                                         19 c
                                                                                                                                                                                                                                                                                Quality: 51.00
Ratio: 4.636
Percent Similarity: 78.571
                                                          .>87
                            .87
                                               /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS S63879
                                                                                                                                                                                                                                                                                                                                               alignment_block:
08-881509-2 x HUMTCRACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_pr8:S63879
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MEDLINE
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/note="Contains the 3' end of the TCRAV/TCRBV, the nDn/n, and the 5' end of the TCRAJ/TCRBJ."
                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS AF043888 51 bp mRNA PRI 11-NOV-1998
DEFINITION Homo sapiens patient CS-1 clone AV228 T cell receptor alpha chain CDR3 (TCR4) mRNA, partial cds.
ACCESSION AF043888.1 GI:3859395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(bases 1 to 51)
Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Selective accumulation of related CD4+ T cell clones in the synovial fluid of patients with rheumatoid arthritis
J. Immunol. 161 (8), 4428-4436 (1998)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (21.JAN-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 51)
Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="T_cell receptor alpha chain CDR3"
/protein_id="AAC72683.1"
/db_xref="GI:3859396"
/translation="YPCAVRISGSARQLFFG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 1
Percent Identity: 73.333
                                                                                                                                                                                                                                                                                                                                       609 ITCTGCGGCACAGCTTCTGGTTCTGCAAGGCAACTGACCTTT 650
                                                                                                                                               Percent Identity: 71.429
                                                                                                                                                                                                                                                                                                 1 .51
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/db_xref="taxon:9606"
/tissue_type="synovial fluid"
/clone="AV228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                      Length:
                                                                                                                             Gaps:
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177 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [TCRAJ22]"
159 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.808
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  197 a
                                                                                                                                                                                               alignment_block: 08-881509-2 x S63879
                                                                                                             Quality:
Ratio:
                                                                                                                                                 Percent Similarity:
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE

MEDLINE JOURNAL REFERENCE AUTHORS JOURNAL

REFERENCE

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Direct Submission
Submitted (17-MAY-1995) Julia L. Hurwitz, Immunology, St. Jude
Children's Research Hospital, 332 N. Lauderdale, Memphis, TN 38101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryotta; Metazoa: Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Metazoa: Arthropoda; Tracheata; Brachycera; Metazoa: Landopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases I to 6822)
Adams, M. D., Celniker, S. E., Holt, R. A., Evans, C. A., Gocayne, J. D., Amanatides, P. G., Scherer, S. E., Li, P. W., Hoskins, R. A., Galle, R. F., Gorge, R. A., Lewis, S. E., Richards, S., Ashburner, M., Henderson, S. N., Brandon, R. C., Rogers, Y. H., Blazej, R. G., Champe, M., Pfeiffer, B. D., Wan, K. H., Doyle, C., Baxter, E. G., Helt, G., Nelson, C. R., Gabor Miklos, G. L., Abril, J. F., Agbayani, A., An, H. J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AE003100 68222 bp DNA INV 06-0CT-2000 COSOSPILIA melanogaster genomic scaffold 142000013385418, complete
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                        1 (bases 1 to 48)
Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L.
Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation
Hum. Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="encodes V alpha 5/J alpha 22 junction"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 90.909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="T-cell receptor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: HSU27254 from: 1 to: 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /isolate="M30"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="blood"
<1. .>48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Drosophila melanogaster
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                                                U27254.1 GI:857594
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  mRNA, partial cds.
U27254
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Percent Similarity: 100.000
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                                                                                                                      Homo sapiens
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08-881509-2 x HSU27254
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                                                                                                  human.
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ORIGIN
                         ACCESSION
                                                                                                                                                                                                               AUTHORS
TITLE
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MEDLINE
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JOURNAL
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KEYWORDS
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                                                VERSION
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                                                                                                                                                                                                                       AF043886 51 bp mRNA PRI 11-NOV-1998
Homo sapiens patient CS-1 clone AV314 T cell receptor alpha chain
                                                                                                                                                                                                                                                                                                                                                                                   Homo saplens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 51)
Strieblich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Selective accumulation of related CD4+ T cell clones in the synovial fluid of pattents with rheumatoid arthritis
J. Immunol. 161 (8), 4428-4436 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Contains the 3' end of the TCRAV/TCRBV, the nDn/n, and the 5' end of the TCRAJ/TCRBJ."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (21-An-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA Location/Qualifiers
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LOCUS HSU27254 48 bp mRNA PRI 10-JUN-1995
DEFINITION Human isolate M30 T-cell receptor V-alpha 5/J alpha 22 junction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 51)
Striebich,C.C., Falta,M.T., Wang,Y., Bill,J. and Kotzin,B.L.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="T cell receptor alpha chain CDR3"
                                                  1 TyrCysLeuVal...LeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                         1 TyrCysLeuVal...LeuSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps: 1
Percent Identity: 73.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="YFCAVRLTGSARQLTFG"
11 c 13 g 17 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="synovial fluid"
/clone="AV314"
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            to: 51
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/db_xref="G1:3859392"
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Align seg 1/1 to: AF043888 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                  AF043886.1 GI:3859391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .>51
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Percent Similarity: 86.667
                                                                                                                                                seq_name: gb_pr3:AF043886
                                                                                                                                                                                           seq_documentation_block:
LOCUS AF043886
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gene

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alignment_block:

BASE COUNT ORIGIN

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Andrews-Pfannkoch,C., Baldwin,D., Ballew,R.M., Basulo,R.Y.,
Baxendale,J., Bayaktaroglu,L., Beasley,E.M., Beeson,K.Y.,
Bancos,P.V., Berman,B.P., Blandari,D., Bolshakov,S., Borkova,D.,
Botos,P.V., Bouck,J., Brokstein,P., Brottier,P., Burtis,K.C.,
Bustam,D.A., Butler,H., Cadleu,E., Center,A., Chandra,I.,
Cherry,J.M., Cawley,S., Danke,C., Davenport,L.B., Davies,P., de
Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M.,
Dodson,K., Doup,L.E., Downes,M., Dugan-Roch,S., Dunkov,B.C.,
Fleischmann,W., Fosler,C., Gabriellan,A.E., Garg,N.S.,
Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z.,
Guan,P., Harris,M., Harris,M.L., Harrey,D., Heiman,T.J.,
Hernandez,J.R., Ketchum,K.A., Kalush,F., Karlen,G.H., Kraft,C.,
Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Rarghon,G.H., Kraft,C.,
I.J.J., Li,Z., Liang,Y., Lin,X., Malush,F., Karlen,G.H., McDerd,M.P., McDerson,D.L., Merkon,G., Milshina,N.V., Mobarry,C.,
I.J.J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
McLeod,M.P., McPherson,D.L., Merkulov,G., Milshina,N.V., Mobarry,C.,
Muzny,D.M., Nebleon,D.L., Nelson,D.R., Nelson,K.,
Nusskern,D.R., Percib,J.M., Palazzolo,M., Pittman,G.S., Pan,S.,
Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Sjeder-Kiamos,I.,
Saungson,M., Strogki,M.P., San,E., Shen,H., Shue,B.C., Sjeder-Kiamos,I.,
Sannpson,M., Strogki,M.P., Shen,H., Shue,B.C., Siden-Kiamos,I.,
Weinstock,G.M., Weissenber,J., Wailliams,S.M., Woodage,T.,
Wenter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
Weinschoff, S., Zhan,M., Zhang,G., Zhan,X., San,K., Shen,J., Shen,J., Shen,J., Sheng,L., Shen,J., Shen,J., Sheng,L., Zheng,L., Zheng,X., Weinsenber,J.S., Zhan,M., Zhong,W., Zhou,S., Zhu,S., Shen,Y., Sheng,L., Sheng,L.,
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RPVNRASSYDSSCYAVNAHPTWTS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
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/db_xref="taxon:7227"
join(<17378. 17578,17630. 17816,17864. >18030)
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join(17378, 17578,17630, 17816,17864, 18030)
/gene="CG18160"
Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4295 others
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is (tastes 1 to 100214)

Birren, B., Fasman, K., McKernan, K., Munro, C., Nusbaum, C.,
Richardson, P., Lander, E., Baldwin, J., Barna, N., Beckerly, R.,
Cantu, C., Castle, A., Chang, A., Cooke, P., Daly, M.J., Deparre, E.,
Devon, K., Dewar, K., Durette, B., Forrest, C., Gage, D., Gardyna, S.,
Gensheimer, S., Geraigery, K., Gilmartin, T., Gray, D., Hagos, B.,
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Jacotoft, L., Linton, L., MacKenzie, J., Marquis, N., McDermott, J.,
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Nachman, A., Naylor, J., O'Connor, T., Olotu, A., Pavlin, B.,
Peterson, K., Roberts, D., Rollins, G., Roy, A., Sarnaik, A., Shiu, P.,
Shyam, R., Stilwell, J., Stone, C., Strickland, C., Sydney, K., Tang, L.,
Direct Submission, 1997) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,

Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,

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Forrest, C., Funke, R. Gage, D., Gardyna, S., Geraigery, K.,

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Maddonald, P., Marquis, W., Morrow, J., Mychalecky, J.,

Mah, R., Naylor, J., Wiloff, M., O'Connor, T., O'Donnell, P.,

Pavlin, B., Peterson, R., Riley, R., Roberts, D., Roy, A., Severy, P.,

Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C.,

Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella Miller, I.,

Ye, W. J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D.,

Ye, W. J., Zhao, J., and Zody, M., Meeler, J., Wu, Y., Wyman, D.,

Direct, Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC003694 186314 bp DNA .ROD 01-SEP-1998
Mus musculus chromosome 19, clone CIT282B21, complete sequence.
AC003694
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Gaps: 0
Percent Identity: 69.231
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/db_xref="taxon:10090"
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/clone="CIT282B21"

48.00

Quality:

alignment_scores:

repeat_region complement(22047. 22237) repeat_region complement(22002. 22398) repeat_region complement(22002. 22398) repeat_region 7.2657. 22850 repeat_region complement(22851. 23042) repeat_region /rpt_family="B2" repeat_region /rpt_family="B2" repeat_region /rpt_family="B3" repeat_region /rpt_family="B3" repeat_region /rpt_family="B3" repeat_region /rpt_family="B3"	/rpt_family="LiMB" /rpt_family="LiMB" /rpt_family="LiM4" /rpt_family="LiM4" /rpt_family="LiM4" /rpt_family="PBID1" /rpt_family="FBID1" /rpt_family="CAGN, /rpt_family="CAGN, /rpt_family="RAINE] /rpt_family="RAINE] /rpt_family="B1-F" /rpt_family="B1-F" /rpt_family="B1-F" /rpt_family="B1-F" /rpt_family="B1-F" /rpt_family="B3" /rpt_family="B3" /rpt_family="B3" /rpt_family="B3" /rpt_family="B1-MM" /rpt_family="B1-MM" /rpt_family="B1-MM" /rpt_family="B1-MM" /rpt_family="B1-F" /rpt_family="B1-F" /rpt_family="B1-F" /rpt_family="B1-MM" /rpt_family="	Ratio: 4.364 Caps:
/clone_lib="Research Genetics/Cal Tech CITB-HSP-C (plates 195-384)" /map="19" /map="19" /chromosome="19" /chromosome="19" /rpt_family="GC_rich" /rpt_family="GC_rich" /rpt_family="GC_rich" /rpt_family="GC_rich" /rpt_family="GC_rich" /rpt_family="GC_rich" /rpt_family="GC_rich" /rpt="single-stranded coverage." /rote="Single-stranded coverage." /rote="Single-stranded coverage." /rote="Probably C."	repeat_region concemigations in this region is ambiguous. repeat_region concemigations (1532, 679) repeat_region concemigations (1532, 679) repeat_region conceming (1542, 1125) repeat_region conceming (1542, 1125) repeat_region conceming (1542, 1125) repeat_region conceming (1542, 1125) repeat_region conceming (1542, 1126) repeat_region conceming (1543, 1136) repeat_region conceming (1546, 1136) repeat_region concement (1546, 1196)	

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polyA_signal
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VERSION
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                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GDB:G00-120-404"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Klein, M.H., Concannon, P., Everett, M., Kim, L.D., Hunkapiller, T. and
                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                    C-region; J-region; T-cell receptor; V-region; antigen receptor; processed gene.
Human peripheral blood lymphocyte, cDNA to mRNA, clone AA27.
                                                                                                                                                                                                                                              HUMTCAZA 183 bp mRNA PRI 13-JAN-1995 HUMTCAZA 184 bp mRNA thuman T-cell receptor active alpha-chain V-region (V-J-C) mRNA, partial cds, clone AA27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="T-cell receptor alpha-chain V-region (V-J-C)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diversity and structure of human T-cell receptor alpha-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                variable region genes
Proc. Natl. Acad. Sci. U.S.A. 84 (19), 6884-6888 (1987)
88016194
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Percent Identity: 81.818
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                                                                                     Align seg 1/1 to: AC003694 from: 1 to: 186314
                                                                                                                                           124522 rggrgttrggrgctctcaggaagcgcgagaga 124554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="14q11.2"
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                                                                                                                          1 TyrCysLeuValLeuSerGlySerAlaArgGln 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /qene="TCRA"
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Chromosome 14q11.2.
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M17666.1 GI:338805
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86.667
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   Percent Similarity: 100.000
                                                                                                                                                                                                  seq_name: gb_pr8:HUMTCAZA
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08-881509-2 x AC003694
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This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X happing Group. Further information can be found at http://www.anger.ac.uk/HGP/ChrX 222D12 is from the library RPC16 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see http://bacpac.med.buffalo.edu/ VECTOR: pPAC4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Mar 24, 1999 this sequence version replaced gi:4469058.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The true left end of clone 393P23 is at 69728 in this sequence. This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure'
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complement(join(1916. .3373,4913. .5084,34073. .34285,
35937. .36099,37414. .37638,44052. .44238,47425. .47637,
51717. .51913,55275. .55411,55801. .55943))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone 22D12. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="match: CDNAs AF059569 AF059611 AF005381 AB020657 AJ012449 AB020657, match: ESTS N64817 N75668 N90812 AA247484 AA054300; supported by GENSCAN and FGENES"
                                                                                                                                                          HS22D12 69827 bp DNA enveloped and chromosome Xq21.1-21.33. Human DNA sequence from clone 22D12 on chromosome Xq21.1-21.33. Contains a novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogenous set of other types of proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (18-MAR-1999) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 69827)
                                                                                                                                                       23-NOV-1999
102 TICTGTGCTGTGACTTTTTCTGGTTCTGCAAGGCAACTGACCTTT 146
                                                                                                                                                                                                                                                                                                 Contains ESTs and GSSs, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                 HTG; KEL; Kelch; Ring Canal protein.
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/clone_lib="RPCI-6"
915. .1335
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                                                                                                                                                                                                                                                                                                                                                                  AL035424.7 GI:4493492
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                                                                           seq_name: gb_pr6:HS22D12
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/// 11034. 11884 / Inches. 1433. .1/31 OL COUSENBUS / 1004. 11884 / Inches. Links 1435. .1/31 OL COUSENBUS / 11034. 11884 / Inches. Links 1.2496 / Inches. Links repeat: matches -775. .154 of consensus. 12451. .14619 / Inches. Links 2. .1580 / Inches. Links 2. .1658 / Inches. Links 2. .16517 / Inches. Inches. 12573. .16517 / Inches. Inches. 126517 / Inches. Inches. 126517 / Inches. Inches. Inches. 12655 / Inches. Inches
                                                                                                                                                            /note="match: proteins CE05435 CE18315 CE01951 CE00627 CE03539 072746 P32206 Q04652 CE14269 CE18133 Q14145 P28575 P21073 P24768 CE06293 073453; supported by GENSCAN and FGENES; start codon could also be on yet unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation-"MNATRSEBQFHVINHAEQTLRKWENYLKEKQLCDVLLIAGHLRI
PAHRLVLSAVSDYFAAMFTNDVLEAKQEEVRMEGVDPNALNSLVQYAYTGVLQIKEDT
IESTLAAACLLQLTQVIDVCSNFLIKQLHPSNCLGIRSFGDAQGCTELLNVAHKYTME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RWDPEGRQWNYVASMSTPRSTVGVYALNNKLYAIGGRDGSSCLKSMEYFDPHTNKWSL
CAPMSKRRGGVGVATYNGFLYVVGGHDAPASNHCSRLSDCVERYDPKGDSWSTVAPLS
VPRDAVAVCPLGDKLYVVGGYDGHTYLNTVESYDAQRNEWKEEVPVNIGRAGACVVVV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HFIEVIKNQEFLLLPANEISKLLCSDDINVPDEETIFHALMQWVGHDVQNRQGELGML
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RDGIKTLNTVECFNTPVGKIMTVMPPMSTHRHGLGVATLEGPMYAVGGHDGMSYLNIVE
                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
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Kelch (Ring Canal protein, KEL) and a heterogenous set of
other types of proteins)"
/protein_id="CAB39994.1"
/db_xref="GI:4539520"
        complement(join(3314. .3373,4913. .5084,34073. .34285,
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51717. .51913,55275. .55411,55801. .55943),
/gene="dAz2p12.1"
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/note="LTR37B repeat: matches 209. .411 of consensus" 7559. .7630
/note="LiMA4A repeat: matches 6222. .6296 of consensus"
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10431. .10738
/note="AluSg repeat: matches 1. .308 of consensus"
10739. .11028
/note="LIMI repeat: matches 1453. .1731 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7631. .7687
Mote-"ITR37B repeat: matches 411. .468 of consensus"
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8/70te="MIR repeat: matches 4. .246 of consensus"
8/78. .2285
7.0ote="Alusx repeat: matches 1. .309 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="MIR_repeat: matches 85. .214 of consensus" 6902. .7200
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/note="Alur repeat: matches 1. 298 of consensus"
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/note="THELB-INTERNAL repeat: matches 1. .1580 of
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/note="29 copies 2 mer ca 85% conserved"
10015. .10430
                                                                                                                                                                                                                                                                                                                                 upstream exon"
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18554. .18
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CDS
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Jelbi. .33314
Jootem.LIPBa repeat: matches -943. .184 of consensus"
3335. .33506
Jootem.LIPBa repeat: matches -1544. .-1372 of consensus"
35655. .35727
Jootem.MERSA repeat: matches 10. .90 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              footem"TIGGER2 repeat: matches 2131. .2185 of consensus"
                                                                                                                                                                                                                                                             38.170...38307
/note="AluSg/x repeat: matches 134. .281 of consensus"
38.2..39082...39465
/note="LIP84 repeat: matches 12. .625 of consensus"
39369...39465
/note="LIP84 repeat: matches 6050..6146 of consensus"
/opene="dA22012.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="match: GSS AQ083204"
40472. .40969
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complement(41258. .41797)
/gene="da22121.1"
/note="match: GSS AQ344849"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /yorbe="match: GSS AQ104504"
42731. .43039
/note="LLTA56 repeat: matches 315. .612 of consensus"
47862. .43761
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L1 repeat: matches 3951. .4196 of consensus"
.19450
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19451. .19738
/note="AluJo repeat: matches 1. .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38061. .38124
/note="MER4-internal repeat: matches 1110. .1171 of
                                                                                                                                                                                                                                                                                                                                                                                /note="AluSx repeat: matches 1. .300 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41401. .41460

/note="30 copies 2 mer tt 73% conserved"

41975. .42030

/note="28 copies 2 mer aa 75% conserved"

complement(42597. .42781)

/gene="dA22D12.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: HS22D12 from: 1 to: 69827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 12
Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43610 TATACATIGGITCTGTCCGGAAACGCGAGACACTC 43575
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91.667
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08-881509-2 x HS22D12/rev
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Ratio:
Percent Similarity:
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i S63879 TCR V alpha -T cell r
i AF043886 Homo sapiens patient
i M17666 Human T-cell receptor
i U83242 Mus musculus D10 T-ce
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1 (bases 1 to 1318)
Jantzer, P. U. and Schendel, D. J.

Ymor-infilltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of a secondary immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J gene; junction; {\tt T} cell receptor; {\tt TCR} junctional sequence; {\tt V} gene. human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
LOCUS HSTCRJUNC 1318 bp mRNA
DEFINITION H.sapiens mRNA for rearranged TCR junctional sequences.
ACCESSION X98410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 12
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <1. .>36
/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                           T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TGCCTCGCTACTGGTTCTGCAAGCAACTGACCTT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="CLATGSARQLTF"
11 c 8 q 11 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CysLeuAlaThrGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="CAB69532.1"
/db_xref="GI:6741523"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unidentified"
/db_xref="taxon:32644"
                                                                                                                                                                       A93133 36 bp DNA Sequence 7 from Patent EP0816496.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: A93133 from: 1 to: 36
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
9
                      142.93
162.31
152.04
141.37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                            A93133.1 GI:6741522
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                        44.50
44.00
44.00
44.00
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Jantzer, P.
                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 36)
Schendel, D.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 5.083
Percent Similarity: 100.000
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                                                                                                                                                   seq_documentation_block:
LOCUS A93133
                                                                                                                                                                                                                                                                    unidentified
                                                                                                                 seq_name: gb_pat1:A93133
                                                                                                                                                                                                                                                                                                          unclassified
                                                                                                                                                                                                                                                                                          unidentified
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                  9b_pr8:S63879
9b_pr3:AF043886
9b_pr8:HUMTCAZA
9b_ro:MMU83242
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                                                                                                                                                                                       DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                              source
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                                                                                                                                                                                                                                                                                                                                               AUTHORS
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                                                                                                                                                                                                                                                                                                                           REFERENCE
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TITLE
                                                                                                                                                                                                                                                  KEYWORDS
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                                                                                                                                                                                                                              VERSION
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ACC10496 Homo sapiens chrome
ACO16595 Homo sapiens chrome
ACC20707 Homo sapiens chrome
ACC23320 Homo sapiens chrome
                                                                                                                                                 -WODEL-frame-from control - DEV-x1p
-WODEL-frame-from control - DEV-x1p
-OG-Cgn2_1/USPTO_spool/DECLOUX-08-881509/runat_28032001_092236_29744/app_query.fasta_1.
-OG-Cgn2_1/USPTO_spool/DECLOUX-08-681509/runat_28032001_092236_29744/app_query.fasta_1.
-OG-Cgn2_1/USPTO_spool/DECLOUX-rege -GAPOP=12.000 -GAPOF=4.500
-USPTO_000 - LGOPCL-0.000 - LGOPEXT-0.000 - FGAPOP=6.000
-GGAPEXT=0.050 - XGAPOP=10.000 - XGAPEXT-0.500 - DELOP=6.000
-FGAPEXT-7.000 - YGAPOP=10.000 - YGAPEXT-0.500 - DELOP=6.000
-FGAPEXT-7.000 - YGAPOP=10.000 - YGAPEXT-0.500 - DELOP=6.000
-FGAPEXT-7.000 - YGAPOP=10.000 - YGAPEXT-0.500 - THR_MIN=0
-ALIGN=15 - NODE-LOCAL -OUTFMT-Pfs - NORM-ext - MINLEN-0
-MAXLEN-200000000 - USER-DECLOUX-08-881509_eGGN1_1_5287
-NCPU-6 - ICPU-3 - LONGLOG - NO_XLPXY - WAIT - THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66 | AE003652 Drosophila melanoga
887 | AE003526 Drosophila melanoga
| L42801 Homo sapiens (clone NSI-H
                                                                            About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              219443
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280887
87 ! L
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OM of: 08-881509-3 to: GenEmbl:* out_format : pfs
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789.70
946.87
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1.2e+03
1.3e+03
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80.80
209.62
124.53
430.58
480.63
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543.25
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2.2e+03
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18.88
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725.56
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199.35
184.34
201.64
190.49
128.80
128.03
125.24
117.81
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105.62
107.47
106.05
105.06
104.15
104.09
103.35
103.35
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136.57
131.66.51
117.07
106.93
103.94
103.94
103.44
103.94
99.47
98.75
96.75
                                                                                                                                                                                                                                                                                                                                                                                                   Query: 08-881509-3
Query length: 13
Database: GenEmbl:*
Database sequences: 1118133
Database length: -1736092196
Search time (sec): 3669.890000
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alignment_scores:
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JOURNAL
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  1. .1318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cells specific for kidney carcinoma patent: EP 0816496-A 07-JAN-1998;
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Sequence 1 from Patent EP0816496.
A93127
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1. .54
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Schendel, D.J.
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BASE COUNT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                   HSU30448 39 bp mRNA PRI 01-AUG-1995 Human isolate M94 T-cell receptor alpha V-J junction (TCR Valpha 3/J alpha 22) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN 38101, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
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Gaps: 0
Percent Identity: 69.231
Length: 13
Gaps: 0
Percent Identity: 84.615
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Percent Similarity: 100.000
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Direct Submission
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                                            92.308
      57.00
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LOCUS HSU30448
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Ratio:
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TITLE
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Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 39)
                                                                      Human isolate M74 T-cell receptor alpha V-J junction (TCR Valpha 3) Jalpha 22) mRNA, partial cds.
                                                                                                                                                                                                                                                     Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L. Restricted usage of T-cell receptor V alpha sequence and variable joining pairs after normal T-cell development and bone
                                                              01-AUG-1995
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Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's
Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Hum. Immunol. 37 (3), 178-184 (1993)
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                                                          mRNA
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AC018245.1 GI:6552946
HTG; HTGS_PHASE2.
                                                      39 bp
                                                                                                                          U30428.1 GI:915481
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seg_name: gb_pr7:HSU30428
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                                 seq_documentation_block:
                                                                                                                                                                                     Homo sapiens
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1 (bases 1 to 92079)

Celniker,S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Butenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolkk,L., Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L., Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E., Pon,K., Man,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
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                                                                                                                                                                                                                                       This sequence was identified as CDM:10214018 by the submitter.
                                                                                                                                                                                                                                                                           For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
                                   Adams.M. and Venter, J.C.
Direct Submission
Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive,
Rockville, MD, UGS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 83677
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/db_xref="taxon:7227"
22418 a 19303 c 19402 g 22554 t
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Gaps: 0
Percent Identity: 83,333
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HTG; HTGS_PHASE1.
fruit fly.
(bases 1 to 83677)
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Percent Similarity: 83.333
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08-881509-3 x AC018245/rev
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                  AUTHORS
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Drosophila melanogaster chromosome 2 clone BACR08114 (D641) RPCI-98
08.1.14 map 60F-60F strain y; cn bw sp, *** SEQUENCING IN PROGRESS
AC007884
On Jul 28, 1999 this sequence version replaced gi:4836864.
For further information about this sequence, including its location and relationship to other sequence, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases. Pl library location:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Pl library, partial Sau3A in pNS582tet14Ad10"
/map="60F1-60F2"
20544 c 20168 g 25194 t 160 others
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Cachiker, S.E., Appayani, A., Arcaina, T.T., Baxter, E., Blazej, R.G., Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L., Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L., Halkle, A., Hoskins, R.A., Huouston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Lee, B., Lewis, S., Li, P., Ling, H., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Pfeiffer, B., Woolley, P., Yang, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D., Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                 525: contig of 525 bp in length 605: gap of unknown length 2501: contig of 1896 bp in length 2581: gap of unknown length 92079: contig of 89498 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Drosophila melanogaster"
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/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                       be preserved.
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• Ratio:
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KEYWORDS
SOURCE
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              COMMENT
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Direct Submission

Direct Submission

Direct Submission

Submitted (21-JUN-1999) Drosophila Genome Center, Lawrence Berkeley

Laboratory, MS 64-121, Berkeley, CA 94720, USA

On Dec 16, 1999 this sequence version replaced 91:5670581.

For further information about this sequence, including its location
and relationship to other sequence, please visit our sequence
archive Web site (http://www.fruitfly.org/sequence/) or send email

to bdgp@fruitfly.Derkeley.edu. All contigs in this submission meet

the following cutoffs: length >= 200 bases.

* NOTE: This is a "working draft" sequence. It currently

* consists of 102 contigs. The true order of the pieces

* is not known and their order in this sequence record is
2 (bases 1 to 130344)
Celniker.S.E., Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G.,
Butenhoff,C., Champe,M., Chavec,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
Kim,E., Lee,B., Lewis,S., Li,P., Lomotan,M.A., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Pfeiffer,B., Poon,L., Sequelra,A., Sethi,H., Snir,E.,
Svirskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zleran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    * arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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7: gap of unknown length
8: gap of unknown length
8: gap of unknown length
9: contig of 1002 bp in length
9: contig of 1002 bp in length
9: contig of 753 bp in length
9: contig of 1005 bp in length
9: contig of 1005 bp in length
9: gap of unknown length
9: gap of unknown length
9: contig of 824 bp in length
9: gap of unknown length
9: contig of 752 bp in length
9: gap of unknown length
9: contig of 752 bp in length
9: contig of 752 bp in length
9: contig of 752 bp in length
9: contig of 1008 bp in length
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of 697 bp in length
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ISM Drosophila melanogaster

Eukaryotes, Macazoa, Arthropoda; Tracheate; Hexapoda; Insecta;

Eukaryotes, Meacazoa, Arthropoda; Tracheate; Brachycera;

Petrygotes, Neoptera; Endopterygote; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (Jaeses It o. 32850)

Adams, M. D., Celniker, S. E., Holt, R. A., Evans, C. A., Gocayne, J. D., Annatides, P. G., Scherer, S. E., Li, P. W., Hoskins, R. A., Galle, R. F., Annatides, R. G., Scherer, S. E., Richards, S., Ashburror, M., Henderson, S. N., Stutton, G. G., Wortunan, J. R., Yandell, M. D., Zhang, O., Chen, L. X., Brandon, R. C., Rogers, Y. H., Blazej, R. G., Champe, M., Pfeiffer, B. Man, K. H., Doyle, C., Baxter, E. G., Helt, G., Nelson, C. R., Gabor, M. Klos, G. L., Abril, J. F., Apbayani, A., An H. J., Basu, A., Bayraktaroglu, L., Beaaley, E. M., Beson, K. Y., Bennan, B. P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M. R., Bouck, J., Brokstein, P., Brottier, P., Buttis, K. C., Busam, D. A., Chandra, I.,
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LOCUS AE003465 328500 bp DNA INV 04-OCT-2000
DEFINITION Drosophila melanogaster genomic scaffold 142000013386038 section 14
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                                                                                                                                                                                                                             bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig of 3693 bp in length
gap of unknown length
contig of 3317 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown length
of 4152 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 12
Gaps: 0
Percent Identity: 83.333
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                                contig of 2201 gap of unknown contig of 4468 bgap of unknown contig of 4468 bgap of unknown gap 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AC007884 from: 1 to: 130344
                                                                                                                                                                                                                                                       unknown ]
of 2671 k
unknown ]
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AE003465 AE002575
AE003465.1 GI:7291836
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71096:
73528:
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                                                                                                                                                                                                                                                                                                                                                                                84048
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Ratio: 5.100
Percent Similarity: 83.333
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08-881509-3 x AC007884
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VERSION
KEYWORDS
SOURCE
ORGANISM
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complement(join(<41090. .41146,41232. ,42191,42248. .>42490))
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/gene="CG13596"
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/qene="CG18510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="FLXBASE:BBan0013596"
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complement(join(29518. 29667,30363. 31091,31485. .31499))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRSATSNINKVKYFVNYKTTOÄRLRRÄGDHAMDATDSHSPLASERPPSTTDDQDVDVSS
TTEEARPEPTLSYSHLHAQEPVLAHQODPREREQEQQEQQQCLEYLGDSAESSPQHLC
GLQSPCHLLERLKVLRLRNCCERSVFSSLHTLALNASLTDRQECVRVLSDLLDVDGLA
NRITCELAEILFRFDCRQVYSLINQCDDCKTRNYGAGWQGREQEQKRRGVHVAVNLWH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKGAEPDRKKERNREAELELDTEAEAGOSNNFISTANNSDPRATDPVISKLOKRSTR
KTEFRKRRIRPCLSVCQTVBOKCPYLLPADRAPALPTOYAGEPTE/CLDOWIPETGA
CLEKSSYGPNDCCYSYCOMPASGICTVCOPGOPGTEREMAGNSTRRVHNITLSLSS
HPGERARAKSYALLARNVSOTGSDPDAVETLLDRLPYYSHDGIFYYDEBGEBRHASL
SGDCAVVPAATTRCTIPYYASGTGAVAKPPTQLLVWLSALLGLLSSCGAARGRWSCOW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MNYISGQCSAGTLPMAWVDEGPGPPTCPRSCAEQQQQKPVASKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSGCGGHRARSRQAVACEANCHEQELVKSRSCSQRSPKVRREKPGQDQDAELVAFRTW
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                                                                                                                                                                                             /evidence=not_experimental
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17430. .17468)
/gene="CG13595"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NANSNASKDIDRSAEEAIDRDLVQTFYDVVGLSKPRHGEEEVLPENEAGLGRSADSEV
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/note="CG18510 gene product"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="CG13596 gene product"
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                                                                                                                   /map="60D10-60D13"
                                                                                       /gene="CG13595"
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   Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doup, L.E., Downes, M., Dugan, Rocha, S., Dunkov, B.C., Dunn, P., Durbin, K.J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Gargin, S., Carrell, J.H., Gu, Z., Galbart, W.M., Glasser, K., Gladek, A., Gong, F., Gorrell, J.H., Gu, Z., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Kenison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C., Kravitz, S., Kulp, D., Lai, Z., Lasko, P., Lei, Y., Levitsky, A.A., Li, J., Li, Z., Liang, Y., Lin, X., Mattei, B., McIntosh, T.C., McIed, M.P., Moshrefi, A., Mount, S.M., Moy, M., Nurphy, B., Murphy, B., Murphy, D.M., Nelson, D.L., Nelson, D.R., Nelson, K.A., Nixon, K., Muszny, D.M., Nelson, D.L., Nelson, D.R., Nelson, P.S., Parlby, J.M., Palazolo, M., Pittman, G.S., Pan, S., Pollard, J., Porly, V., Reese, M.G., Rehnert, K., Remington, K., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Stupski, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R., Worley, K.C., Wu, D., Yang, S., Wang, Z.Y., Wassarman, D.A., Worley, K.C., Wu, D., Yang, S., Wang, Z.Y., Wassarman, D.A., Worley, K.C., Wu, D., Yang, S., Zhu, X., Smith, H.O., Gibbs, R.A., Myers, E.W., Rubin, G., Zhao, Q., Zheng, L., Zheng, X.H., The genome sequence of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALVSSAGSLAGSKLGRFIDTHDIVMRPNHAPTOGHEVDVGSKTTIRVVNSQVVTKPEF DFTRRPIRANTIAAMDPGKYNGTLEDMLTSADYDLFSNYELYRRYPKSRAFLIDPH SVWRLWQSLQMFAGNRPISKNPPSSGFIGLALLLPHCPQVDFVEYVPSTRLNGRCHYY SKEMNSACTFGSWHPLAAEKLMALDMNMAEDDDMSVFOFGILRIRRPDKLLCGFNFFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(<15236. .16209,16271. .16428,16497. .17101,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SKNTKLTLSTKLYLCHDKHSELCHNKTQQFRQRIVRAFEKAMVESVNESQANHYNVDY
KPVFGDSFEEQYYPSTCLVMEAGVRVLRRKDAPFNKLPFGRLFPRQKLFRNVKDIKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 328500)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(7434. .7604,7668. .7765,7873. .8152,8215. .8312,8567. .9109,9179. .>9440))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA Location/Qualifiers
1. 328500
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8215. .8312,8567. .9109,9179. .9344))
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                 TITLE
JOURNAL
                                                                                                                   FEATURES
                                                                                 COMMENT
AC005350 78661 bp DNA PRI 31-JUL-1998
Homo sapiens chromosome 5, BAC clone 261j17 (LBNL H190), complete
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 78661)
Kimmerly,W., Bondoc,W., Cheng,J., Connolly,K.S., Gunning,K.M., Kadner,K., Miguel,T., Miller,C., Pitluck,S., Pollard,M., Sequencing of human chromosome 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Large Scale Sequence Analysis and Annotation with the Sequence Comparison Analysis (SCAN) System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kimmerly W., Bondoc, M., Cheng, J., Connolly, K.S., Gunning, K.M., Davis, C.A., Kadner, K., Miguel, T., Pitluck, S., Pollard, M., Rojeski, H., Subramanian, S. and Martin, C.H.
                                                                                                                                                                                        QPGTGTDLQSSGISVSLCLSKTLYSL"
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/gene≂"CG9189"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 83,333
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join(53150. .53722,54265. .54357)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AE003465 from: 1 to: 328500
                                                                                                                                                                                                                                                                                                                                                                                                              /note="CG9189 gene product"
/codon_start=1
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                                                                                                                                                                                                                                                                                                            /gene="CG9189"
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AC005350
AC005350.1 GI:3366562
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Ricke, D.O.
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5.100
83.333
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LOCUS AC005350
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Ratio:
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KEYWORDS
SOURCE
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AUTHORS
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Direct Submission
Submitted (31-JUL-1998) Human Genome Center, DOE Joint Genome
Institute, Lawrence Berkeley National Laboratory, MS 74-157,
Berkeley, CA 94720, U.S.A.
Sequence submitted by:
DOE Joint Genome Institute.
Location/Qualifiers
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47b___656

2704__2839

7note="GRAIL 2 excellent exon, frame 0"

4504. .4592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="GRAIL 2 excellent exon, frame 2" complement(30575, 30784)
/note="GRAIL 2 excellent exon, frame 0" 31846. 31869
/note="(TA)12"
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/rpt_unit=AC
/rpt_unit=AC
/rpt_unit=AC
/note="GRAIL 2 excellent exon, frame 0"
39883. .40023
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complement(15044, 15135)
/rpt_family="MIR"
complement(16072, 16399)
/rpt_family="Line"
19038, 19075
                                                                                                                                                                                                                                                                                                                                                                                                                         /rpt_family="MLT2B2"
9398. .10759
/rpt_family="L1"
complement(10780. .14299)
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/rpt_family="Alu"
complement(29199, 29244)
                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/map="5q"
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complement(34387..3
/rpt_family="MER3"
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24716. 24995
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25177. 27648
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8089. .8226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_unit=AT
complement(19076.
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36735. .36764
/note="(AC)15"
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rpt_family="L1"
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/rpt_unit=T
                                                                                                                                                                                                     /clone="261j17"
                                                                                                                                                                                                                       /chromosome="5"
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/note="(T)21"
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                                                                                                                              1 .78661
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a 14357 c 14140 g 24597 t
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/rpt_family="L1"
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                                                                                                                                                                                                                                                              /rpt_family="MLT1"
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57577 57507
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complement(65010, .66136)
/rpt_family="L1"
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complement(66461. .66710)
/rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complement(70474. .70725)
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complement(72044. .72130)
/rpt_family="L1"
complement(40416. .40487)
/rpt_family="MER44C"
41142. .41292
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/rpt_unit=AG
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56543. 56706
                                                                                  /rpt_family="Alu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="(GT)15"
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                                                                       .41837
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75291. .76794
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92.308
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08-881509-3 x AC005350
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Ratio:
Percent Similarity:
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Consensus quality: 185896 bases at least Q40
Consensus quality: 197156 bases at least Q30
Consensus quality: 197156 bases at least Q30
Consensus quality: 199406 bases at least Q20
Estimated insert size: 194000; agarose-fp estimation
Estimated insert size: 204969; sum-of-contigs estimation
Quality coverage: 8.57 in Q20 bases; agarose-fp estimation
Quality coverage: 8.11 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 30 contigs. The true order of the pieces
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Submitted (29-JUN-2000) Mitchell Drive, Walnut Creek, CA 94598, USA
------Genome Center
Center: Joint Genome Institute
                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
1 (20786)
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 207869)
DOE Joint Genome Institute.
                                                                           29-JUN-2000
                                                                         AC073697 207869 bp DNA HTG 29-JUN-20
Mus musculus clone RP23-161111, WORKING DRAFT SEQUENCE, 30
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1715: gap of unknown length
3062: contig of 1347 bp in length
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seq_name: gb_htg17:AC073697
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                                                        seq_documentation_block:
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unknown length

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JOURNAL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 23126)
DOE Joint Genome Institute.
Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS AC073735 231260 bp DNA HTG 18-JUL-2000
DEFINITION MUS musculus clone RP23-25C2, WORKING DRAFT SEQUENCE, 24 ordered
                                                                                                                                                                                                                                                                                                    gap of unknown length
contig of 7715 bp in length
gap of unknown length
contig of 10027 bp in length
gap of unknown length
contig of 13476 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="RPCI mouse BAC library 23"
48520 c 48115 g 55879 t 2907 others
                                                                                                                                                             g or ...
if unknown lengtn
ig of 6039 bp in length
...known length
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155225: gap of unknown length
207869: contig of 52644 bp in length.
                                                                                                                                                                                                                                   10267 bp in length
                          bp in length
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contig of 7909 bp in length
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contig of 5336 bp in length
gap of unknown length
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                                               contig of 4082 ago of unknown l contig of 4467 b gap of unknown l contig of 8783 b gap of unknown l
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gap of unknown 1
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gap of unknown 1
contig of 3330 k
gap of unknown ]
contig of 5801 k
gap of unknown ]
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/db_xref="taxon:10090"
/clone="RP23-161111"
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AC073735.2 GI:9256774
HTG: HTGS_PHASE2; HTGS_DRAFT.
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Consensus quality: 217735 bases at least 040
Consensus quality: 226530 bases at least 040
Consensus quality: 226530 bases at least 030
Consensus quality: 227843 bases at least 020
Estimated insert size: 239600; agarose-fp estimation
Estimated insert size: 239600; agarose-fp estimation
Cuality coverage: 7.12 in 020 bases; agarose-fp estimation
Quality coverage: 7.39 in 020 bases; sun-of-contigs estimation
* NOTE: This is a working draft' sequence. It currently
* consists of 24 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
                                                           Direct Submission

Submission

Submission

Submission

Submission

Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jul 18, 2000 this sequence version replaced 91:8810352.

Center: Joint Genome Institute

Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           * This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

* 8749 848: gap of unknown length
* 8612 36012 contig of 8748 bp in length
* 8649 36011 contig of 27163 bp in length
* 43919 44018: gap of unknown length
* 43919 44018: gap of unknown length
* 46191 48586: contig of 7868 bp in length
* 46867 64952: contig of 16266 bp in length
* 4687 64952: contig of 16266 bp in length
* 65053: gap of unknown length
* 65053: gap of unknown length
* 67087: contig of 16363 bp in length
* 67087: contig of 5835 bp in length
* 70888 70987: gap of unknown length
* 70888 107221: contig of 36234 bp in length
* 70888 107221: contig of 36234 bp in length
* 70888 107221: contig of 16686 bp in length
* 70988 107221: contig of 16686 bp in length
* 70888 107221: contig of 67868 bp in length
* 70878 70987: gap of unknown length
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of 11598 bp in length
unknown length
of 3096 bp in length
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unknown length
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of 1675 bp in length
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                                                                                                                                                                                                                                                                                                      Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                       Center Project Name: 1746522
Center clone name: RPCI-23_25C2
2 (bases 1 to 231260)
DOE Joint Genome Institute.
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gap of
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186705:
                                                                                                                                                                                                                                                                                                                                                                      Project Information
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ELVVPPKPIQNAFDSISYFRDAWLRKLSHKGQVLKSSIADVVACYSSEKRKLYQKAAD
                 SLEKKPVQWÄDSKVQAFIKVEKLECDTKDPVPRTIQPRSKRYNLVIGQYLRLNEKKML
DAIDDVFGEKTVLSGLDNRAQGRAIAHKWRKYQNPIGIGLDASRFDQHCSVDALKFEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
1 8026 c 7649 q 9103 t
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Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                         923 t
                                                                                                                                                                                                      /protein_id="AAA47457.1"
/db_xref="GI:310361"
                                                                                                                                                   2424. .3440
/standard_name="ORF3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3511 TACTGTTTGGCAACAGGGTCGGCGAGA 3485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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LOCUS AC014160 34220 bp D:
DEFINITION Drosophila melanogaster,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 TyrCysLeuAlaThrGlySerAlaArg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster
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HTG; HTGS_PHASE2.
                                                                                                                                                                                        /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Percent Similarity: 100.000
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08-881509-3 x SCWFUSPRO/rev
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Ratio:
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ORIGIN
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SOURCE
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                                                                                                                                                       CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MGFISESLFDVDKLLVWVSKFNPGKILSSICNLGVDCWNRFRKW
FFGLNFDAHWMAVDAFWLLDFWTEGDFWRVDDFCSETGESKLEDCELDFSVNBFFD
EEVYRDEEGWWVLQFTSSKHIRRYRAGMAQAAIRAVERTINRHTIFGDDMGKVDE
AAVRATASDIGGEFKINEHHTWVLVYAAAYLAMTPDQRSIDSVKLAYNPKSQARRTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="MKSKRVVGLPAVSAGLKVCVHQTSLHNMIVSLERRVFRVKNAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sweet clover necrotic mosaic virus (strain 59) RNA.
Sweet clover necrotic mosaic virus
Sweet clover necrotic mosaic virus
Viruses; ssRNA positive-strand viruses, no DNA stage;
Tombusvirides, Dianthovirus.

1 (bases 1 to 3876)
Ge,Z., Hiruki,C. and Roy,K.L.
Wucleotic sequence of Sweet clover necrotic mosaic dianthovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sweet clover necrotic mosaic virus unidentified genes, three complete cds's including fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sweet clover necrotic mosaic virus"
/strain="59"
/db_xref="taxon:28348"
   200238: contig of 13533 bp in length 200338: gap of unknown length 206497: contig of 6159 bp in length 20855: gap of unknown length 208755: contig of 2158 bp in length 208855: gap of unknown length 231260: contig of 22405 bp in length.
                                                                                                                                                                                                                                 /clone_lib="RPCI mouse BAC library 23"
52031 c 52510 g 62847 t 2307 others
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                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 84.615
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121. .831
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/protein_id="AAA47456.1"
/db_xref="GI:310360"
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/protein_id="AAA47455.1"
/db_xref="GI:310359"
                                                                                                                                                                         /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-25C2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /standard_name="ORF1"
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                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AC073735 from: 1
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4.042
92.308
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LOCUS SCWFUSPRO
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                                                                                 206598
208756
208856
                             200239
200339
                                                                    206498
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Ratio:
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                                                                                                                                                                                                                                                      BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
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VERSION

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KPTKAALHTQIVLSVVGSIALHANNGKASQRFRLIDSSNPALFPTIAYFAANYDMYRMK
KLTLRYVPLVTVQNGSRVAMTWDPDSQDSVPQSRQBISAYSRSSISTAVYEKCSLTIPP
DWGRRFADSSNVDRKLVYGQLLFVNHSGSEGIETGDYFLECEVEFKGPOPTATVVO
RGIIDDRGVLTGEGFSYLLPTDTGIEVNHLDVAGTYLVTLVYTSSGSGRAUQVLG
NSTLVGDFRTAXSGINFIATFTGISMULDVAGTYLVTLVYTSSGSGRAUQVLG
TEYRECFPGDOLEOLIKWOLTNIGSALLPFGCELVRYRTKVGRMSGDINTGLGONKILM
CSMVHAFLKETGVRASLANNGDDCVLFCEKGDYEGINRULEDWFLCRSFEMTVEKPVD
VLEKVVPCRSOPVCLATOWANTROLEGISRDCFSTODMLINPKTFKDAMNALGCONGII
NDGVPFHMAGAKLMHKSAFTGSSIWRGLHKOMEYRNRRDRLGKRTNLLWSEVEDATRLS
YFRAFSIEPVVQRIVUEEYLSOVEVTCEGRETNVLPTHYSRIHKDLIKSR"
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*** SEQUENCING IN PROGRESS ***, in ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MSTKAPKKSKQRSKPRNRNPSTSVKTVTIPFAKTQIVKTVNPPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence was identified as CDM:10210117 by the submitter. For further information on this sequence e-mail to fly@celera.com. * NoTE: This is a 'working draft' sequence. * This sequence will be replaced * by the finished sequence as soon as it is available and * the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 34220)
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contig of 932 bin length gap of unknown length contig of 1167 bp in length gap of unknown length length contig of 1444 bp in length gap of unknown length gap of unknown length contig of 1648 bp in length gap of unknown length gap of unknown length gap of unknown length contig of 1832 bp in length gap of unknown length contig of 1832 bp in length contig of 838 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2197: gap of unknown length
22276: contig of 1079 bp in length
2326: gap of unknown length
2316: contig of 805 bp in length
2324: gap of unknown length
2324: gap of unknown length
24101: contig of 860 bp in length
24101: contig of 880 bp in length
2524: gap of unknown length
2524: gap of unknown length
2524: gap of unknown length
26781: contig of 1537 bp in length
26806: contig of 1199 bp in length
28140: gap of unknown length
28140: gap of unknown length
28550: contig of 1109 bp in length
28561: gap of unknown length
30734: gap of unknown length
                                                                                                                                                                                                    contig of 1000 bp in length gap of unknown length contig of 1177 bp in length contig of 589 bp in length gap of unknown length contig of 884 bp in length contig of 884 bp in length gap of unknown length
                               contig of 494 bp in length sigh of unknown length contig of 547 bp in length sigh of unknown length sigh of 682 bp in length sigh of unknown length contig of 608 bp in length sigh of unknown length sigh of unknown length
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gap of unknown length
contig of 1035 bp in length
gap of unknown length
contig of 1245 bp in length
gap of unknown length
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gap of unknown length
contig of 1364 bp in length
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contig of 1383 bp in length
gap of unknown length
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of 1035 bp in length
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gap of unknown length
contig of 1227 bp in length
gap of unknown length
contig of 954 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown length
of 1245 bp in length
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of 1386 bp in length
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of 2258 bp in length
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contig
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For further information about this sequence, including its location archive Web site (http://www.fruitfly.org/sequence, including its location to bdggefruitfly berkeley.edu. All contigs in this submission meet to bdggefruitfly berkeley.edu. All contigs in this submission meet ** NOTE: This is a 'Working draft' sequence. It currently ** is not known and their order in this sequence record is ** arbitrary. Gaps between the contigs are represented as ** This record will be updated with the finished sequence ** as soon as it is available and the accession number will **
                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AC007648 130184 bp DNA HTG 02-MAR-2000
DEFINITION Drosophila melanogaster chromosome 3 clone BACR13A02 (D705) RPCI-98
13.A.2_map 88E-88F strain y; cn bw sp, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pierygota; Neoptera; Findopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilade; Drosophila (bases 1 to 130184)

Celniker,S.E., Apbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Buttenhoff,C., Champe,M., Chavez,C., Chew,M., Ciesiolka,L., Hinkle,A., Forkina, E., Galle,R., George,R.A., Harris,N.L., Hinkle,A., Hoskins,R.A., Houston,K.A., Hummasti,S.R., Karra,K., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Woolley,P., Yang,S., Sethi,H., Svirskas,R., Wan,K.H., Webster,D., Sequencing of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 130184)
2 (bases 1 to 130184)
2 (bases 1 to 130184)
Butenhoff.C. Champe,M., Chavez,C., Chew,M., Ciesiolka,L.,
Doyle,C.M., Farfan,D.E., Galle,R., George,R.A., Harris,N.L.,
Klm,E., Lee,B., Lewis,S., Li,P., Lomotan,M., Mazda,P.,
Moshrefi,A.R., Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S.,
Stelffer,B., Poon,L., Sequeira,A., Sethi,H., Snir,E.,
Syliskas,R.R., Wan,K.H., Weinburg,T., Zhang,R., Zieran,L.L. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      contig of 619 bp in length

; gap of unknown length

; contig of 969 bp in length

; gap of unknown length

; contig of 1068 bp in length

; gap of unknown length

; contig of 748 bp in length

; gap of unknown length
                                                                                                                            Align seg 1/1 to reverse of: AC014160 from: 1 to: 34220
Ratio: 4.273 Gaps: 0
Percent Similarity: 91.667 Percent Identity: 75.000
                                                                                                                                                                                              6686 TTTTGCTTGGCTGTCGCCTCGGCTCGGCAGCAACA 6651
                                                                                                                                                                         1 TyrCysLeuAlaThrGlySerAlaArgGlnLeuThr 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster
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3644:
3724:
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                                                               alignment_block:
08-881509-3 x AC014160/rev
                                                                                                                                                                                                                                                             seq_name: gb_htg1:AC007648
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KEYWORDS
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JOURNAL
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JOURNAL
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contig of 3240 bp in length as contig of 3240 bp in length as contig of 3388 bp in length agap of unknown length agap of unknown length contig of 5181 bp in length contig of 535 bp in length agap of unknown length contig of 5879 bp in length agap of unknown length agap of un
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g of 668 bp in length
f unknown length
g of 598 bp in length
f unknown length
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gap of unknown length
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of 641 bp in length
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unknown length
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unknown length
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                                                                     gap of unknown length contig of 2015 bp in length gap of unknown length
                                                                                                                                                      gap of unknown length
contig of 1832 bp in length
                                                                                                                                                                                                                unknown length
of 2226 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown length
contig of 2182 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
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contig of 501 bp in length
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                                                               contig of 1164 bp in length
gap of unknown length
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of 1722 b
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of 1314 h
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of 2427 l
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117653
118286
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114802
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49221: gap of unknown length
50737: contig of 1516 bp in length
50817: gap of unknown length
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12

Length: Gaps:

alignment_scores:
Quality: 47.00
Ratio: 4.273

Percent Identity: 75.000 Percent Similarity: 91.667

alignment_block: 08-881509-3 x AC007648

Align seg 1/1 to: AC007648 from: 1 to: 130184

gene,

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i U29953 Human pigment epith
i AC004897 Homo sapiens PAC
i AC004695 Homo sapiens BAC
i AC034147 Homo sapiens chr
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LVSGSARQLTFGXCLDSGSARQLTFGXCLVSGSARQLTFGXCLA
TGSARQLTFGXCLOGGDTDK.LFGXCLVLSGSARQLTFGXCLVLSGSARQLTFGXCLV
VSGSARQLTFGXCLALGGSARQLTFGXCLALAGSARQLTFGXCLAPSGSARQLTFGXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1. :>1318
// Onte="V gene/J gene junction"
// Codon_start=1
// product="TCR junctional sequence"
// Protein_id="CAA67057.1"
// Ab_xref="IL:170561"
// translation="CLVGSSAROLTFGXCLATGSARQLTFGXCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVAGGGNTPLVFGXCLVGGSARQLTFGXCLVGGSARQLTFGXCLVGRSARQLTFGXCL
TAGSARQLTFGXCLVGAGGYQKVTFGXCLVLSGSARQLTFGXCLVAPGGATNKLIFGX
CLVVLGGSGQNLIFGXXLVGPNNAGNMLTFGXXCLVATNGGRNCSDLW"
329 c 334 t 87 others
                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa; Chordata; Vertebrata; Mammalia; Butheria; Primates; Catarhini; Hominidae; Homo.
1 (bases 1 to 1318)
Jantzer, P.U. and Schendel, D.J.
Tymor-infiltrating lymphocytes recognizing spontaneously arising renal call carcinomas express T cell receptors characteristic of secondary immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION Human isolate M94 T-cell receptor alpha V-J junction (TCR Valpha ACCESSION U30448
                                                                                                                                                                                                                                                                      J gene; junction; T cell receptor; TCR junctional sequence; V human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
                                                                                                                                                                                      08-JAN-1997
                                                                                                                                                                 HSTCRJUNC 1318 bp mRNA PRI 08-JJ
H.sapiens mRNA for rearranged TCR junctional sequences
X98410
       22484
90731
149572
163015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 12
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .1318
/organism="Homo sapiens"
/isolate="patients 22 and 26"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 TGCCTCGACTCCGGTTCTGCAAGGCAACTGACCTTT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: HSTCRJUNC from: 1 to: 1318
       365.69
1.5e+03
2.6e+03
2.8e+03
       1113.47
102.26
98.24
97.55
                                                                                                                                                                                                                                                     X98410.1 GI:1770560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
2 (bases 1 to 1318)
Jantzer, P.
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         44.00
44.00
44.00
44.00
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Ratio: 5.167
Percent Similarity: 100.000
                                                                                                                  seq_name: gb_pr7:HSTCRJUNC
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                                                                                                                                                            seg_documentation_block:
LOCUS HSTCRJUNC
DEFINITION H.sapiens mRN
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       gb_pr7:HSU29953
gb_pr1:AC004897
gb_pr1:AC004695
gb_htg13:AC034147
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AUTHORS
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JOURNAL
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1318 i x99410 H.sapiens mRNA for rear
39 | U30448 Human isolate M94 T-cell
39 | U30428 Human isolate M94 T-cell
39 | U30428 Human isolate M74 T-cell
36 | A93133 Sequence I from Patent EF
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2611 | Y00750 Sheep mRNA for prostagla
2666 | J03999 Sheep prostaglandin G/H
4912 | AFT11086 Bos taurus latrophili
4989 | AFT11089 Bos taurus latrophili
5046 | AFT11087 Bos taurus latrophili
5041 | AFT11090 Bos taurus latrophili
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184881 | AC06198 Homo sapien
                                                                                                                                                                   Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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OM of: 08-881509-5 to: GenEmbl:*
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Database: GenEmbl:*
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Search time (sec): 3669.890000
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9b_pat1:A93127

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9b_pat1:A93133

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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bummalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 39)

Dave, V.P., Larche, M., Rencher, S.D., Koop, B.F. and Hurwitz, J.L.

Restricted usage of T-cell receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation

Hum. Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                                                                                                                                                  Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JAN-2000
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Percent Identity: 76.923
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Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
Location/Qualifiers
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Schendel, D.J.
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U30448.1 GI:915515
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Percent Similarity: 100.000
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08-881509-5 x HSU30448
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SSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLMSS"
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1 (bases 1 to 39)

Dave, V. P., Larche, M., Rencher, S. D., Koop, B. F. and Hurwitz, J. L. Restricted usage of Treel1 receptor V alpha sequence and variable-joining pairs after normal T-cell development and bone marrow transplantation

Hum. Immunol. 37 (3), 178-184 (1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSU30428 39 bp mRNA PRI 01-AUG-1995
Human isolate M74 T-cell receptor alpha V-J junction (TCR Valpha
3/J alpha 22) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (22-JUN-1995) Julia L. Hurwitz, St. Jude Children's
Research Hospital, Immunology, 332 N. Lauderdale, Memphis, TN
38101, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="T-cell receptor alpha V-J junction"
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Gaps: 0
Percent Identity: 84.615

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/gene="TCR Valpha 3/J alpha 22"
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    /isolate="M74"

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Align seg 1/1 to: G39068 from: 1 to:
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                                                              Unpublished (1998)
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                  and Fishman, M.C.
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08-881509-5 x G39068
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AUTHORS
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211968 Zebrafish AB Danio rerio STS genomic, sequence tagged site.
G39068
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                        Length: 13
Gaps: 0
Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 83.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="unnamed protein product"
/codon_start=1
                                                                                                                                                                                1 TICTGTGCTACTTCTGGTTCTGCAAGGCAACTGACCTTT 39
                                                                                                                                                              1 TyrCysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 36)
Schendel, D.J.
T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="CAB69532.1"
/db_xref="GI:6741523"
/translation="CLATGSARQLTF"
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    .36
    /organism="unidentified"
    /db_xref="taxon:32644"

                                                                                                                                                                                                                                                               DEFINITION Sequence 7 from Patent EP0816496.
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91.667
                                     4.818
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unidentified
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LOCUS A93133
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08-881509-5 x HSU30428
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Percent Similarity:
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Percent Similarity:
                        Quality:
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/dev_stage="Adult"
/lab_host="DH5alphaF'IQ"
/lab_host="DH5alphaF'IQ"
/note="Vector: ml3MP19 with added BatXI site; V-type:
Phage: Genomic DNA from a single adult zebrafish of AB
strain was digested with Alui, Cac8!, HaeIII, NIaVI, or
Rsal. Fragments in the range of 250-500 bp were gel
purified and a BatXI linker was added. The fragments were
cloned into a modified M13mp19 vector and transformed
into E. Coli DH5alpha. Microsatelliite sequences were
screened with labeled d(CA)15 and d(GT)15 oligonucleotide
                                                                                                                                Contact: Mark C. Fishman
Cardiovascular Research Center
Massachusetts General Hospital
Mail code 1494100A, 149 13th Street, Charlestown, MA 02129, USA
Fax: 6177265806
Shimoda, N., Knapik, E.W., Ziniti, J., Sim, C., Yamada, E., Kaplan, S
                                                 A genetic linkage map of the zebrafish with 2000 microsatellite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 others
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                                                                                                                                                                                                                                                                                                                                                                                                                        Presook:
94 degrees C for 5.0 minutes
Denaturation: 94 degrees C for 1.0 minute
Annealing: 58 degrees C for 1.0 minute
Polymerization: 72 degrees C for 1.5 minute
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Gaps: 0
Percent Identity: 69.231
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Location/Qualifiers
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50 mM
10 mM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR Cycles: 27
Thermal Cycler: MJ Research PTC-100
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                                                                                                                                                                                                                                                                     Email: fishman@mgh.cvrc.harvard.edu
http://zebrafish.mgh.harvard.edu
Primer A: TGTGGAGGACACAGTGTGF
Primer B: TGCACAGTAACCACTCAGC
STS size: 147
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 ng
each 375 nM
each 200 uM
: 0.034 units/ul
10 ul
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/clone_lib="Zebrafish AB"

    604
    /organism="Danio rerio"

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160 g
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Tris-HCl:
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237. .256
complement(364. .
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08-881509-5.rge

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REFERENCE
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/product="mature prostaglandin endoperoxide synthase (AA 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SWISS PROT:P05979"
/translation="MSRQSISLRFPLLLLLLSPSPVFSADPGAPAPVNPCCYYPCQHQ
GICVRFGLDRYQCDCTRTGYSGPNCTIPEIWTWLRTTLRPSPSFIHFLLTHGRWLWDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tanabe,T.
Submission
Submitted (05-APR-1988) Tanabe T., National Cardiovascular Center
Research Institute, 5-7-1 Fujishiro-dai, Suita, Osaka 565, Japan
Research Institute, 5-7-1 Fujishiro-dai, Suita, Osaka 565, Japan
C. (1848) Takai,T. and Tanabe,T.
Primary Structure of sheep prostaglandin endoperoxide synthase
PERS Lett. 231 (2), 347-351 (1988)
88196421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae;
                                                                                                                                                                                                                                                                23-MAR-1995
                                                                                                                                                                                                                                                                                                   Sheep mRNA for prostaglandin endoperoxide synthase.
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469. 471
/note="pot. N-linked glycosylation site"
1267. .1269
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149. .351
                                                                                                                                                                                                                                                                                                                                                                                                             prostaglandin endoperoxide synthase; synthase.
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                                   1 TyrCysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9940"
/tissue_type="vesicular gland"
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/db_xref="G1:1362"
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743 c 707 g
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40. .11
112. .1839
Troduct-'mature peptide of prostaglandin endo
peroxidase'
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40. .1844
/product='prostaglandin endo peroxidase of
                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Artiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae; Caprinae;
                                                                                                                                                                                                                                                                                         29-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA CODING PROSTAGLANDIN ENDOPEROXIDE SYNTHETASE PATENT: JP 1989228479-A 1 12-SEP-1989; MEIJI MILK PROD CO LTD
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                                                                                                                             Align seg 1/1 to reverse of: OAPGES from: 1 to: 2611
                                                                                                                                                                                                                                                                                         cDNA encoding prostaglandin endo peroxidase. E02077
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Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 75.000
Length: 12
Gaps: 0
Percent Identity: 75.000
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Key Location/Qualifiers
                                                                                                                                                                                    1150 TGCCTAAATTCCGGATCAACTAGAAATCTGACATTC 2115
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/organism="Ovis aries"
/db_xref="taxon:9940"
a 746 c 705 g 65
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strandedness: Double;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               topology: Linear;
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anti-sense: No;
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JP 1989228479-A/1.
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Ratio: 4.000
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08-881509-5 x E02077/rev
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08-881509-5 x OAPGES/rev
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LOCUS
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FKTRQGQMAKQPCPAGTIGVSTYLCLAPDGIWDPQGPDLSNCSSPWVNHITQKLKSGE TAAMIAREIAEQTRNHINAGDITYSYRAMDQIVGLLDVQLRNLTPGKKDSAARSLUKL QKRRSCRAYVQAWVETVNNLLQPQALNARDLITSDQLRATMLLDTVEESAFVLAD NLLKTDITVERNTDNICLEVARLSTEGNLEDLKFPENTGHGSTIQLSNNTLKQNGRNGE IRVAFVLYNNLGPYLSTENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLAD NICISLFVAELLFLIGINRTDQPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEV FESEHSRRKYFYLVGYGMPALLVAVSAAVDYRSYGTDKVCWIRLDTYFIWSFIGPATL ITMINVIFLGIALYKMFHTAILKPESGCLDNIKSWVIGATALLCLLGLTWAFCLMYI NESTVIMAYLFTIFLSLQCMFIFIHOVLOKKVREYGKCLÆTHCCSGRSTESSIGSG KTSGSRTPGRYSTGSQSRIRRWWNDTVRKQSESFITGDINSSASLNREPYRETSMGV POVEPDPCPGTYKYLEVQYECVPYKVEOKVFLCPGLLKGVYOSEHLFESDHOSGAMCK DPLQASDKIYYMPWTPYRTDTLJFYSSKDDFIAGRPTTTYKLPHRVDGTGFVVYDGAL FFNKERTRNIVKFDLRTRIKSGEAIIANANYHDTSPYRWGGKSDIDLAVDENGLWYIY ATEQNNGKIVISQLNPYTLRIEGTWDTAYDKRSASNAFWICGILYVVKSVYEDDDNBA TROKIDYIYWTDQSROSLVDVPPPRYSYQIAANDYNRPRONILLYWWNYKTHYVKYSLDEG PLDSRSGQAHGGVGYTSPPTHLDSDLERPPYREISTTGPLGTGSTTTFTTWS PGRSTTPSVSGRRNRSTSTPSPAIEVLNDITTHVPSASPQIPALBESCEAVEAREIMW PVVFTVKHIKQSEENFNPNCSFWSYSKRTMTGYWSTQGGRLLTTNKTHTTCSCNHLTN FAVLMAHVEVKHSDAVHDLLLDVITWVGILLSLVCLLICIFTFCFFRGLQSDRNTIHK /translation="MWPSQLLVFMMLLAPIIHAFSRAPIPMAVVRRELSCESYPIELR CPGTDVIMIESANYGRTDDKICDSDPAQMENIRCYLPDAYKIMSQRCNNRTQCAVVAG Bos taurus Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea; Bovidae; Bovinae; Bos. Submitted (04-DEC-1998) Biochemistry Department, Imperial College, Exhibition Road, London SW7 2AY, UK Location/Qualifiers 1 (bases 1 to 4912) Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A. He latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution FEBS Lett. 443 (3), 348-352 (1999) /evidence=experimental /product="latrophilin 3 splice variant abag" /protein.id="hatrophilin 3 splice variant abag" /db_xref="GI:4164055" 2 (bases 1 to 4912) Matsushita, H., Lellanova, V.G. and Ushkaryov, Y.A. Direct Submission 1. 4912 /organism="Bos taurus" /db_xref="taxon:9913" 164. 3859 /codon_start=1 AF111086 AF111086.1 GI:4164054 4939 bp 48.00 4.364 84.615 alignment_block: 08-881509-5 x AF111086/rev seq_name: gb_om:AF111089 Quality: Ratio: Percent Similarity: 99148828 1390 alignment_scores: ORGANISM ACCESSION VERSION KEYWORDS SOURCE BASE COUNT REFERENCE AUTHORS JOURNAL REFERENCE AUTHORS JOURNAL CDS FEATURES TITLE TITLE ORIGIN DSFRYGPODYSYEQFLENTSHLVDYGVEALVDAFSROPAGRIGGGRNIDHHILHVAVD VIKESRVLRLOPFNEYRKRFGMKPYTSFQELTGEKEMAAELEELYGDIDALEFYPGLL LEKCHPNSIFGESMIEMGAPFSLKGLLGNPICSPEYWKASTFGGEVGFNLVKTATLKK /protein_id="AAA31576.1" /db_xref="G1:166036" /translation="MSRQSISLRFPLLLLLLSPSPVFSADPCAPAPVNPCCYYPCQHQ TPMGTKGKKOLPDAEFLSRRFILLRRFIPDPQGTNLMFAFFAQHFTHQFFKTSGKMGP GFTRALGKOVDLGHIYGDNLERQYQFLRFKDGKLKYQMLNGBYYPPSVBEBYVLMHYP RGIPPQSQMAVGQFYGLLLFGLMLTATURLBHNRVODLLKAHHPWGDGDCLFGTARL ILIGETIKIVIEBYVQQLSGYFLQLKFDPELLFGAQFQYRNRIAMEFNOLYHMHPLMP GICVRFGLDRYQCDCTRTAIPAPTAPSRRYGPGSGRLCGPAPLSSTFMLTHGRWLWDF VNATFIRDTLMRLVLTVRSNLIPSPPTYNIAHDYISWESFSNVSYYTRILPSVPRDCP Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Povidea; Caprinae; Ovis. 1 (bases 1 to 2666) DeWitt,D.L. and Smith,W.L. Primary structure of prostaglandin G/H synthase from sheep Primary structure of prostaglandin G/H synthase from sheep Proc. Natl. Acad. Sci. U.S.A. 85, 1412-1416 (1988) Draft entry and computer-readable sequence for [1] kindly provided seq_documentation_block: LOCUS AF111086 4912 bp mRNA MAM 04-MAR-1999 DEFINITION Bos taurus latrophilin 3 splice variant abag mRNA, complete cds. 27-APR-1993 prostaglandin G/H synthase signal peptide" /note="prostaglandin G/H synthase precursor (EC SHPPGS 2666 bp mRNA MAM 27 Sheep prostaglandin G/H synthase mRNA, complete cds J03599 prostaglandin synthase. Sheep vesicular gland, cDNA to mRNA, clone PGHS-ov. /note="prostaglandin G/H synthase mRNA" LVCLNTKTCPYVSFHVPDPRQEDRPGVERPPTEL" 165. .1892 Gaps: 0 Percent Identity: 75.000 165. .. 1892 /note="prostaglandin G/H synthase" 760 c 737 g 628 t 2150 TGCCTAAATTCCGGATCAACTAGAAATCTGACATTC 2115 2205 TGCCTAAATTCCGGATCAACTAGAAATCTGACATTC 2170 2 CysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13 Align seg 1/1 to reverse of: SHPPGS from: 1 /organism="Ovis sp." /db_xref="taxon:9939" by D.L.Dewitt, 19-JAN-1988. Location/Qualifiers /codon_start=1 1.14.99.1)" J03599:1 GI:166035 .1895 .164 Ratio: 4.000 Percent Similarity: 100.000 1. .2666 /note=' alignment_block: 08-881509-5 x SHPPGS/rev seq_documentation_block: LOCUS SHPPGS seq_name: gb_om:AF111086 seq_name: gb_om:SHPPGS Unreported. Quality: Ratio: Ovis sp. alignment_scores: sig_peptide mat_peptide source DEFINITION ORGANISM JOURNAL MEDLINE COMMENT BASE COUNT REFERENCE AUTHORS **MRNA** ACCESSION VERSION KEYWORDS SOURCE PEATURES TITLE ORIGIN

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to: 4912
                                                                                                                      Length: 13
Gaps: 0
Percent Identity: 69.231
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KLNIAYQIGASEQCQGYKCHGYSTTEW"
1153 c 1091 g 1278 t
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TAANIA RELAECTRINILINAGDITY SVRAMDQLVGLLIDVQLRIN. ITPGGKDSAÄRSLINKL
OKRERSCRAYVQAWFETVNILLQPQALNAMRDLTTSDQLRAATWLLDTVEESAFVLAD
ILKTDIVRENTDNIQLEVARLSTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGE
IRVAFVLYNILGPYLSTENSAMKLGTEAMSTRHSVIVNSPVITAAIINEFSKRYYLAD
PVVFTVKHIKQSEENFUNDLSFRASSYKKGTEAMSTRHSVIVNSPVITAAIINEFSKRYTLAD
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/db_xref="GI:4164061"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLDSRSGQAHHGOVSYISPPIHLDSDLERPPVREISTTGPLGTGSTTTSTTLRTTTWS
PGRSTTPSVSGRRNRSTSTPSPAIEVLNDITTHVPSASPQIPALEESCEAVEAREIMW
FKTRQGQMAKOPCPAGTIGVSTYLCLAPDGIWDPQGPDLSNCSSPWVNHITQKLKSGE
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TWAFGLMYINBSTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVRKEYGKCLRTHCCSGR
STESSIGSGKTSGSRTPGRYSTGSQSRIRRMNDTVRKQSESSFITGDINSSASLNRE
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DPLQASDKIYYMPWTPYRTDTLTEYSSKDDFIAGRPTTTYKLPHRVDGTGFVVYDGAL
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TGNKIDYIYNTDQSKDSLVDVPFPNSYQYIAAVDYNPRDNLLYVWNNYHVVKYSLDPG
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NLCISLFVAELLFLIGINRTDQPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEV
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                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
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Direct Submission
Submitted (04-DEC-1998) Biochemistry Department, Imperial College,
Bos taurus latrophilin 3 splice variant abbg mRNA, complete cds.
                                                                                                                                                                                                                                                                                 Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A. He Latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution FEBS Lett. 443 (3), 348-352 (1999)
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/db_xref="taxon:9913"
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08-881509-5 x AF111089/rev
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FKTROGOMAKOPCPAGTIGVSTYLCLAPDGIWDPQGPDLSNCSSPWVNHITQKLKSGE
TAANIARELAEQTRNHLNAGDITYSVRAMDQLVGLLDVOLRNLTPGGKDSAARSLNKL
QKRERSCRAYVQAMYETVNNLLQPQALNAWRDLITSDQLRAATMLLDTVEESAFVLAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NILKTDIVRENTDNIQLEVARLISTEGNLEDLKFPENTGHGSTIQLSANTLKQNGRNGE
IRVAFVLYNNLGPYLSTENASMKLGTEAMSTNHSVIVNSPVITAAINKEFSNKVYLAD
PVVFTVKHIKQSEENFNPNCSFWSYSKRTMTGYWSTQGCRLLTTNKTHTTCSCNHLTN
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KTSGSRTPGRYSTGSQSRIRRMWNDTVRKQSESSFITGDINSSASLNRGAMANHLISN
ALLRPHGTNNPYNTLLGEPAVCNNPSVSMYNAQEGLLNNARDTSVMDTLPLNGNHGNS
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DPLQASDKIYYMPWTPYRTDTLTEYSSKDDFIAGRPTTYKLPHRVDGTGFVVYDGAL
FFNKERTRNIVKFDLRTRIKSGEAIIANANYHDTSPYRWGGKSDIDLAVDENGLWVIY
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PLDSRSGQAHHGQVSYISPPIHLDSDLERPPVREISTTGPLGTGSTTTSTTLRTTWS
PGRSTTPSVSGRRNRSTSTPSPAIEVLNDITTHVPSASPQIPALEESCEAVEAREIMW
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NKLVNNLGSGSEDDAIVLDDATSFNHEESLGLELIHEESDAPLLPPRVYSTENHQLHH
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PPAKCGDAEDVYYKSMPNLGSRNHVHQLHTYYQLGRGSSDGFIVPPNKDGTPPEGSSK
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                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
Direct Submission
Submistica (04-DEC-1998) Biochemistry Department, Imperial College,
Exhibition Road, London, SW7 2AY, UK
AF111085 4989 bp mRNA MAM 04-MAR-1999
Bos taurus latrophilin 3 splice variant abaf mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                     Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
The latrophilin family: multiply spliced G protein-coupled
receptors with differential tissue distribution
FEBS Lett. 443 (3), 348-352 (1999)
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/db_xref="taxon:9913"
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                                                                                      AF111085.1 GI:4164052
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KEYWORDS
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1 TyrCysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13

Bos

ORGANISM

KEYWORDS SOURCE

AUTHORS TITLE

REFERENCE

MEDLINE REFERENCE

JOURNAL

AUTHORS JOURNAL

TITLE

DEFINITION

sed_name:

ACCESSION VERSION

5016

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DPLQASDKIYYMPWTPYRTDTLTEYSSKDDFIAGRPTTTYKLPHRVDGTGFVVYDGAL
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TROUNGKI TU ISOLNPYTRIEGTWDTAYDKRSASANEMIGCILYVVKSYFBDDDBAR
TGNKIDY IX WIDOSKOSIVDPPEPNSYQY TAANDY NEPDNLLYVWNYHVYKYSLDFG
PLDSRSGQAHHGQVSY ISPPIHLDSDLERPPVREISTTGPLGTGGSTTTFTTLATTTAFT
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FRIRGGOMAKQPPCAGT IGVSTYLLCLAPDITHVPSASPOIRALESCEAVENEIM
TAANIARELAEQIRNHLNAGDITYSVRAMDQLVGLLDVOLRNLTPGKLKSGE
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INLATULYBRYDDIQLEYARLSTEGRUEDLKFPBNTGHGSTTQLSARTLKONGRNGE
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PVVFTVKHIKQSEENFNPNCSFWSYSKRTWTGYWSTQGCRLLTTNKTHTTGSCNHLTN
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NLCISLFVAELLFLIGINRTDQPIACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEV
FESEHSRRKYFYLVGYGMPALIVAVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATL
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KTSGSRTPGRYSTGSQSRIRRMWNDTVRKQSESSFITGDINSSASLNRCAMANHLISN
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
Direct Submission
Submitted (04-DEC-1998) Biochemistry Department, Imperial College,
                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
LOCUS AF111087 5041 bp mRNA MAM 04-MAR-1999
DEFINITION BOS taurus latrophilin 3 splice variant abah mRNA, complete cds.
ACCESSION AF111087
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Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A.
The latrophilin family: multiply spliced G protein-coupled
Teceptors with differential tissue distribution
FEBS Lett. 443 (3), 348-352 (1999)
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/protein_id="Ath05323.1"
/db_xref="GI:4164057"
                                                                                                                                                                                                                                                   1 TyrCysLeuAspSerGlySerAlaArgGlnLeuThrPhe 13
                                                                                                                           Align seg 1/1 to reverse of: AF111088 from: 1
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/db_xref="taxon:9913"
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Location/Qualifiers
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            alignment_block:
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/product-"latrophilin 3 splice variant abbf"
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/db_xref="GI:4164059"
/translation="WWPSQLLVFWMLLAPIIHAFSRAPIPMAVVRRELSCESYPIELR
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TWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVPKEYGKCLRTHCCSGR
STESSIGSGKTSGSRTPGRYSTGSQSRIRRMWNDTVRKQSESSFITGDINSSASLNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDVFPDPCPGTYKYLEVQYECVPYKVEQKVFLCPGLLKGVYQSEHLFESDHÖSGAWCK
DPLQASDKIXYMPWTPYRTDTLTEYSSKDDFIAGRPTTTYKLPHRVDGTGFVVYDGAL
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FESEHSRRKYFYLVGYGMPALIVAVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATL
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SSEQNRNLANKLVNNLGSGSEDDAIVLDDATSFNHEESLGLELIHEESDAPLLPPRVY
STENHQLHHYTRRRIPQDHSESFFPLLTNEHTEDLQSPHRDSLYTSMPALAGVPTAES
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Mammalla, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (04-DEC-1998) Biochemistry Department, Imperial College, Exhibition Road, London SW7 2AY, UK Locatlon/Qualifiers
                                                                                                                                                                                                 AF111088 5016 bp mRNA MAM 04-MAR-1999
Bos taurus latrophilin 3 splice variant abbf mRNA, complete cds.
AF111088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 5016)
Matsushita.H., Lelianova.V.G. and Ushkaryov,Y.A.
He latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution
FEBS Lett. 443 (3), 348-352 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matsushita,H., Lelianova,V.G. and Ushkaryov,Y.A. Direct Submission
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2077 CATTGCCTGGACATAGGCTCTGCAAGAGCGCTCTTTT 2039
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/db_xref="taxon:9913"
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FEATURES

13

Gaps: Length:

alignment_scores:

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ATEQNICATIVE SQLIPYTLE LEGTWDT AYDKREA SNA FWICGLLYVVK SVY EDDDNEA TGRKI DY INTDOSKDS LVDV FPRISY OF LAAVDY REBULLYVWNYTHVYK YSLDFG TGRKI DY INTDOSKDS LVDV FPRISY OF LAAVDY REPULLIFYWNNYTHVYK YSLDFG PGRSTTPS TRATTTWS PGRSTTPS VSGRRARTSTSTE BEATEV LND ITH HVPSA, SPQ IPALESC CEAVEREINW FKTROGOMAKOPCPACTIGVSTYLLCLAADGINDD SQPDLLSNCSSPWYNHITYCKLKSGE
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NLLKTDIYVRRYDNIQLEVARLSTEGALEDLKPPRITGHSTIQLSANTLLKQNGNNGE
IRVAFVIX NNLGPYLETRASMKLGTERAMSTHHSVI INSPYTTAAINKEFSNKYLLAD
PVYFTYKHIKQSEBRIPRNGSFWSYSKRTMTGYWSTQGCRLLTINKTHTTCSCNHLTN
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TWAFGLMYINESTVIMAYLFTIFNSLQGMFIFIFHCVLQKKVRKEYGKCLRTHCCSGR
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PDVFPDFCPGTYKYLEVQYECVPYKVEQKVFLCPGLLKGVYQSEHLFESDHQSGAWCK
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AMANHLISNALLRPHGTNNPYNTLLGEPAVCNNPSVSMYNAQEPYRETSMGVKLNIAY
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission Submission Submitted (04-DEC-1998) Biochemistry Department, Imperial College, Exhibition Road, London SW7 2AY, UK Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AFT11090 5068 bp mRNA MAM 04-MAR-1999
DEFINITION BOS taurus latrophilin 3 splice variant abbh mRNA, complete cds.
ACCESSION AF111090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A. Matsushita, H., Lelianova, V.G. and Ushkaryov, Y.A. The latrophilin family: multiply spliced G protein-coupled receptors with differential tissue distribution FEBS Lett. 443 (3), 348-352 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="latrophilin 3 splice variant abbh"
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Matsushita,H., Lelianova,V.G. and Ushkaryov,Y.A.
                                                                                                                                                              Align seg 1/1 to reverse of: AF111087 from: 1 to: 5041
   Percent Identity: 69.231
                                                                                                                                                                                                                                                           2077 CATTGCCTGGACATAGGCTCTGCAAGAGCGCTCTCTTT 2039
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1195 c 1121 g 1
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Percent Similarity: 84.615
                                                                    alignment_block: 08-881509-5 x AF111087/rev
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JOURNAL
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1435

BASE COUNT ORIGIN

alignment_scores:

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Align seg 1/1 to reverse of: AF111090 from: 1 to: 5068
Length: 13
Gaps: 0
Percent Identity: 69.231
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84.615
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08-881509-5 x AF111090/rev
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1. 1318
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/isolate="patients 22 and 26"
/db_xref="taxon:9606"
              3.8e+03
3.9e+03
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A93131
              95.19
95.07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
2 (bases 1 to 1318)
Jantzer, P.
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           gb_htg23:AP001980
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1318 | x98410 H.sapiens mRNA for rear 39 | A93131 Sequence 5 from Patent EF 42 | AJ23520 Homo sapiens mRNA for T 1341 | A93127 Sequence 1 from Patent EF 7 | L42801 Homo sapiens (clone N31-F 214 | U40776 Human T-cell receptor al 716 | S63879 TCR V alpha "T cell receptor al 51 | AF004388 Homo sapiens patient CS 98 | S69140 TCR V alpha "T cell recept 177580 | AC05515 Homo sapiens chromo 187137 | AC017084 Homo sapiens chromo 187419 | AC069155 Homo sapiens chromo 17581 | AC069159 Homo sapiens chromo 17581 | AC06918 Homo sapiens chromo 17581 | AC01640 Homo sapiens chromo 17581 | AC01648 Homo sapiens chromo 17581 | AC0188 Homo sapiens chromo 17581 | AC0188 Homo sapiens chromo 17581 | AC0188 Homo sapiens chromo 201502 | AC01348 Homo sapiens chromo 201502 | AC01348 Homo sapiens chromo 201502 | AC013017 Homo sapiens chromo 124508 | AL139017 Homo sapiens chromo 201605 | AC05605 Homo sapiens chromo 201600 | AC05605 Homo sapiens chromo 201605 | AC
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-O-(cgn2_1/USPPO_spool/DECLOUX-08-881509/runat_28032001_092236_29744/app_query.fasta_1.
-DB-GGnEmbl -QFMT-fastap -SUFFIX=rge -GAPOP-12.000 -GAPEXT-4.000
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                                                                                                           About: Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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Search time (sec): 3669.890000
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Sequence
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/product="TcR junctional s
AP001980 Homo sapiens
AL356112 Homo sapiens
AC027539 Homo sapiens
AC018429 Homo sapiens
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J gene; junction; T cell receptor; TCR junctional sequence; V gene.
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Eukaryota; Metazoa; Chordata; Vertebrata; Mammalla; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1318)
Jantzer, P. U. and Schendel, D. J.
Thumor-infiltrating lymphocytes recognizing spontaneously arising renal cell carcinomas express T cell receptors characteristic of secondary immune response
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Submitted (11-JUN-1996) P. Jantzer, Institute for Immunology,
Goethestr. 31, D- 80336 Munich, FRG
Location/Qualifiers
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H.saplens mRNA for rearranged TCR junctional sequences.
X98410
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167960
169801
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Crossreactive recognition of viral, self, and bacterial peptide ligands by human class I-restricted cytotoxic T lymphocyte clonotypes: implications for molecular mimicry in autoimmune
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 42)
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Misko,I.S., Cross,S.M., Khanna,R., Elliott,S.L., Schwidt,C.,
Pye,S.J. and Silins,S.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 96 (5), 2279-2284 (1999)
99162595
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/note="unnamed protein product"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CysLeuValValSerGlySerAlaArgGlnLeuThrPhe 14
                                                                                                   T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
                                                                                                                                                                                                                                                                                                              /translation="CLVLSGSARQLTF"
                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
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    .39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: A93131 from: 1 to: 39
                                                                                                                                                                                                   /db_xref="taxon:32644"
                                                                                                                                    BOEHRINGER MANNHEIM GMBH (DE)
                                                                                                                                                       Location/Qualifiers
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AJ235208.1 GI:3851223
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                                                                 1 (bases 1 to 39)
Schendel, D.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                   61.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: gb_pr6:HSA235208
                unidentified.
                                  unidentified
unclassified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross, S.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block: 08-881509-6 x A93131
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AUTHORS
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KEYWORDS
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ORIGIN

SOURCE

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SQSKDSDV1IDKTVLDMRSWLFKSNSAVARSNKSNFRSDFACANAFNNSIIPEDTFFPSPE
SSCDVKLVEKSFETDTNLNFQNLSVIGFRILLLKVAGFNLLMTLRLWSS"
                                                                                                                                                                                                                                                                                                                                                                                                                                          22-JAN-2000
                                                                                                                               Length: 13
Gaps: 0
Percent Identity: 84.615
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                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 1341)
Schendel, D. J.
T-cells specific for kidney carcinoma
Patent: EP 0816496-A 07-JAN-1998;
BOEHRINGER MANNHEIM GMBH (DE)
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                                   16
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/db_xref="taxon:32644"
1. .54
1. .804
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/cell_line="SP1"
1..42
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LOCUS A93127
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unclassified
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alignment_scores:
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                                                      AUTHORS
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                                                                                                                                                                                                                                                             Clonal expansion of myelin basic protein-reactive T cells in patients with multiple sclerosis: restricted T cell receptor V gene rearrangements and CDR3 sequence Eur. J. Immunol. 25 (4), 958-968 (1995)
                                                                                                                                                                                                                               Vandevyver, C., Mertens, N., van den Elsen, P., Medaer, R., Raus, J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS HSU40776 214 bp mRNA PRI 07-DEC-1995
DEFINITION HUMAN T-cell receptor alpha chain (TCRAV2S1J22) mRNA, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 214)

Kurnick,J.T., Ihara,A., Pervaiz,S., Pandolfi,F., Van,Den Elsen P., Waltkus,K., Boyle,L.A., Hishii,M. and Andrews,D.M.

T-cell receptor usage by anti-melanoma specific cytotoxic tumor-infiltrating lymphocytes. Detection of dominant tumor-specific T-cell clones by single strand conformational polymorphism and T-cell receptor
                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 87)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Partial TCRVA (1. .15), TCRNA (16. .18), TCRJA (19. .75), partial TCRCA (76. .87)" /codon_start=1
HUWTCRACG 87 bp mRNA PRI 07-NOV-1995
Homo sapiens (clone NSI-:F4) T cell receptor alpha chain (TCRA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product-"T cell receptor alpha chain"
/protein_id="AAA80064.1"
/db_xref="G1:853663"
/translation="YFCASGSRQLTFGSGTQLTVLPDIQK"
19 2 1 9 27 t
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                                                                              L42801.1 GI:853662
T cell receptor alpha.
Homo sapiens (clone: NS1-F4) cDNA to mRNA.
Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="NS1-F4"
/map="14411.2"
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                                           mRNA, partial cds.
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                                                                                                                      SOURCE
                   DEFINITION
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                                                             ACCESSION
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KEYWORDS
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/product-"T-cell receptor alpha chain"
/protein_id="AAAB3012.1"
/db_xref="G1:11013937"
/translation-"SIYSNGDKEDGRFTAQLNKASOYVSLLIRDSQFSDSATYLCAVN
SGSARQLIFGSGTQITVLPDIQNPDPA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Manmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I bases 1 to 716)
Griesinger, F., Jansen, B. and Kersey, J.H.
Differentiation in mature T lymphold leukemia cells is unstable and reversible to myeloid cells, without the involvement of a common
                  2 (bases 1 to 214)

Variation, Tr., Thara, A., Pervaiz, S., Pandolfi, F., Van, Den Elsen P., Waitkus, R., Boyle, L.A., Hishii, M. and Andrews, D.M.

Direct Submission

Direct Submission

Direct Submission

Laboratory, Massachusetts General Hospital, 149 East 13 St., Charlestown, MA 02129, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCR V alpha =T cell receptor variable alpha chain (human, MT-ALL, Genomic Mutant, 716 nt).
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                                                                                                                                                                                                                                                                                                                               /cell_type="cytotoxic T-cell lymphocyte"
1. .214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 13
Gaps: 0
Percent Identity: 84.615
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                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MU 57"
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/db_xref="taxon:9606"
                                                                                                                                                                                               Location/Qualifiers
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/note="TCR V&agr"
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9
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09
Unpublished (1995)
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08-881509-6 x HSU40776
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08-881509-6.rge

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source
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                                                                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
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Bukaryota; Metazoa; Arthropda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Nascomorpha; Ephydroidea; Drosophilidae; Drosophila.

I (bases 1 to 66222)

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D.,

Adams, M.D., Celniker, S.E., Richardas, S., Ashburner, M., Henderson, S.N.,

Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, O., Chen, L.X.,

Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D.,

Man, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor

Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J.,

Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A.,

Baxendale, J., Bayraktaroglui, Ballew, R.M., Basu, A.,

Benos, P.V., Berman, B.P., Blandari, D., Bottier, P., Burtis, K.C.,

Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I.,

Cherry, J.M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de

Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M.,

Dodson, K., Doup, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C.,

Dunn, P., Durbin, K.J., Evangelista, C.C., Ferrazo, C., Ferriera, S.,

Galbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell, J.H., Gu, Z.,

Guan, P., Harris, M., Harris, N.L., Harvey, D., Heiman, T.J.,

Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C.,

Li, J., Li, Z., Liang, Y., Lin, X., Mattei, B., McIntosh, T.,

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Muzny, D.M., Nesher, D.L., Nelson, D.R., Nelson, K.A., Nuxon, K.,

Nusskern, D.R., Parleo, J.M., Palazzolo, M., Pittman, G.S., Pan, S.,

Palaso, M., Panleo, L., Nelson, D.R., Nuxon, K.,

Nusskern, D.R., Panleo, J.M., Palazzolo, M., Pittman, G.S., Pan, S.,
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YSGTYPGGSSTOLTVLDDIONPDBAVYQL"
159 c 177 g 183 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE003100 68222 bp DNA INV 06-0CT-2000 Drosophila melanogaster genomic scaffold 142000013385418, complete
join(58 ..109,340...>716)
/gene="TRK V alpha"
/note="This sequence comes from Figure 4: conceptual
translation presented here differs from translation in
publication"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            609 TICTGCGGCACAGCTICTGGTTCTGCAAGGCAACTGACCTTT 650
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Percent Identity: 71.429
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LOCUS AE003100
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ORIGIN
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SOURCE
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                                         CDS
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Pollard, J., Puri, V., Reese, M.G., Reinert, K., Remington, K., Saunders, R.D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I., Sidenson, M., Stupski, M.P., Smith, T., Spier, E., Spradling, A.C., Stapleton, M., Strong, R., Sun, E., Spierskas, R., Tector, C., Venter, E., Wang, A. H., Wang, X., Wang, Z. Y., Wassarman, D.A., Weinstock, G. M., Weissenbach, J., Williams, S. M., Woodage, T., Worley, K.C., Wu, D., Yang, S., Yao, O.A., Ye, J., Yeh, R.F., Zaveri, J.S., Zhan, M., Zhang, G., Zheng, L., Zheng, X., Shith, H.O., Gibbs, R.A., Myers, B.W., Rubin, G.W. and Venter, J.C.
The genome sequence of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NEVHRSPPQQASHVGVPYPRLPQRVGQQVGQEPISGMISQKPPPIPGQGIPCKSSLAA
SIPTSPSESAAPASATDSGQPNCPSAAGQFCTDESGLRWRTYARWIHSGPVFWHFKPA
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                                                                                                                                                                                                                                                                                                                                         20196006
20196006
2.0 (bases Leo 68222)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J.
Direct Submission
Submitted (21 MAR-2000) Celera Genomics, 45 West Gude Drive,
Rockville, MD, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .17578,17630. .17816,17864. .>18030)
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join(17378. .17578,17630. .17816,17864. .18030)
/gene="CG18160"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18042 a 13196 c 12804 g 19885 t 4295 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 0
Percent Identity: 76.923
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="FlYBASE:FBan0018160"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CG18160"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="CT40964"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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4.250
92.308
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08-881509-6 x AE003100/rev
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Ratio:
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Molecular basis of cross-reactivity among allergen-specific human T cells T-cell receptor V alpha gene usage and epitope structure Immunology 81 (1), 15-20 (1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Contains the 3' end of the TCRAV/TCRBV, the nDn/n, and the 5' end of the TCRAJ/TCRBJ." /codon_start=1
                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 51)
Striebich,C.C.; Falta,M.T.; Wang,Y.; Bill,J.; and Kotzin,B.L. Selective accumilation of related CD4+ T cell clones in the 3ynovial fluid of patients with rheumatoid arthritis J. Immunol. 161 (8), 4428-4436 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="from rheumatoid arthritis patient CS-1 [TCRAV1S3]
[TCRAJ22]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 98) Mohapatra, S.S., Mohapatra, S.S.,
                                                                                                                                                                                                                                                                                                                                                                      C (bases 1 to 51)

Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L.

Striebich, C.C., Falta, M.T., Wang, Y., Bill, J. and Kotzin, B.L.

Direct Submission

Submitted (21-JAN-1998) Pediatrics, National Jewish Medical and Research Center, 1400 Jackson St., Denver, CO 80206, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human peripheral blood grass-sensitive individual VI 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="T_cell receptor alpha chain CDR3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="synovial fluid"
/clone="AV228"
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    .51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="TCRA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="TCRA"
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86.667
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                                            Homo sapiens
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08-881509-6 x AF043888
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SOURCE
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ESM Homo sapiens
EURaryota; Metazoa: Chordata; Craniata; Vertebrata: Euteleostomi;
Bukaryota; Metazoa: Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 17750)

8 Muzny, D.M., Adams, C., Balley, M., Barbaria, J., Blankenburg, K.,
Bodota, B., Bouck, J., Davie, S., Brooks, A., Bunay, C., Bunac, C.,
Burkett, C., Burrows, J., Cater, M., Chacko, J., Chen, Z., Cox, C.,
Burkett, C., Durrows, J., Cater, M., Ding, Y., Domah-Rashid, N.,
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Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, J. H., Gorrell, J., Gorvern, Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,
Relly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLecd, M. P., Mei, G., Morgan, N.,
Morris, S., Nash, S., Neslson, A., Naguen, N., Nauyen, N., Nayen, S.,
Cabal, C., Parish, B., Paxton, S., Payton, B., Perez, L., Pu, L.,
Tabor, P., Shen, H., Simon, M., Samuel, S., Say, J., Scherer, S.,
Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, Q., Wabbah, M.,
Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A.,
Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
                                                                                                                                                                                                                                                                                                                                                                        /gene="TCR V alpha"
/note="This sequence comes from Fig. 3b; Protein sequence
is in conflict with the conceptual translation"
GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 144562] from the original journal article. This sequence comes from Fig. 3a.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /exception="Protein longer than coding region shown; mismatch(12[E->G])" /product="T-cell receptor alpha-chain" /protein_id="AAB30244.1" /db_xref="G1:545974" /translation="DSATYFCAALPESAROLTFGSGTQLTVLPDIQN"
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AC069515
                                                                                                                                                                                                                                                             /gene="TcR V alpha"
/note="T-cell receptor alpha-chain"
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Gaps: 0

Percent Identity: 64.286
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                                                                                                                 1. .98
/organism="Homo sapiens"
/db_xref="taxon:9606"
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37561 c 36782 g 50297 t
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gap of unknown l
contig of 1227 b
gap of unknown l
contig of 1325 b
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gap of unknown 1
contig of 1474 b
gap of unknown 1
contig of 1157 b
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gap of unknown l
contig of 3360 b
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gap of unknown l
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/db_xref="taxon:9606"
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NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                     Submitted (02-UNN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 5, 2000 this sequence version replaced gi:8705299.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17112: contig of 17112 bp in length
17212: gap of unknown length
29649: contig of 12437 bp in length
29749: gap of unknown length
39046: contig of 9297 bp in length
39146: gap of unknown length
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unknown length
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Contact: hgsc-help@bcm.tmc.edu
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Gibbs, Kubmission
Unpublished
2 (bases 1 to 17580)
Worley, K.C.
Direct Submission
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123347:
                                                                                                                                            Center code: BCM
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Direct Submission
Submitted (09-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jul 7, 2000 this sequence version replaced gi:8568870.
Homo sapiens chromosome 2 clone RP11-480F1, WORKING DRAFT SEQUENCE,
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 183137) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. The true order of the places is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://genome.wustl.edu/gsc/index.shtml
Center project Information
Center project name: H. W10480F01

Center project name: H. W10480F01

Sequencing vector: M13; 71%
Sequencing vector: M13; 71%
Sequencing vector: plasmid; 29%
Chemistry: Dye-primer ET; 71% of reads
Chemistry: Dye-terminator B19 Dye; 29% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 17680 bases at least Q30
Consensus quality: 178737 bases at least Q20
Insert size: 190000; agarose-fp
Insert size: 182277; sum-of-contigs
Quality coverage: 4.93 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
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gap of unknown length
contig of 7318 bp in length
gap of unknown length
contig of 10601 bp in length
gap of unknown length
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gap of unknown length
contig of 13119 bp in length
gap of unknown length
contig of 11582 bp in length
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gap of unknown length
contig of 60765 bp in length
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                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                              AC017084.5 GI:8954420
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Waterston, R.H.
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                                                            AC017084
                 DEFINITION
                                                                                                                                            ORGANISM
                                                                                                                                                                                                     REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                 JOURNAL
REFERENCE
AUTHORS
                                                          ACCESSION
                                                                                  VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                      JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                       SOURCE
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/organism="Homo sapiens" /db_xref="taxon:9606"

Location/Qualifiers

source

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Eukaryotta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryotta; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1. (bases 1 to 187419)

2. I (bases 1 to 187419)

3. Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,
Bodota, B., Bouck, J., Bowie, S., Brooks, A., Buhay, C., Bunac, C.,
Burkett, C., Burroway, J., Carter, M., Chen, Z., Cox, C.,
David, R., Delgado, O., Deshazo, D., Ding, Y., Domah-Rashid, N.,
Dugan-Rocha, S., Durbin, K. J., Fernandez, C., Ferraguto, D.,
Forcum-Tansey, J., Frantz, P., Ganesh, R., Gorrell, L.L.,
Guevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,
Holloway, C., Hosak, H., Jackson, L.E., Jackson, L., Jia, Y., Jia, Y., Lu, S.,
Kelly, S., Kondejewski, N., Kong, Y., Kovar, C., Leal, B., Li, Z.,
Lichtarge, O., Liu, J., Liu, W., Logan, O., Lozado, R.J., Lu, J.,
Lucier, R., Martin, R., Martinez, C., McLeed, M.P., Mel, G., Morgan, M.,
Oswal, G., Parish, B., Paxton, S., Nash, S., Sander, S., Shah, E., Shen, H., Simon, M., Sparks, A., Stamps, A., Sucgang, R.,
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HOMO Sapiens chromosome 3 clone RP11-568NI, WORKING DRAFT SEQUENCE,
18 unordered pieces.
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Percent Identity: 83.333
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                                             /clone="RP11-480F1"
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HTG: HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                     vector_side:right"
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/chromosome="2"
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                                                                                                                                                                        clone_end: T7
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Percent Similarity: 91.667
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LOCUS AC069255 18
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08-881509-6 x AC017084
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TITLE JOURNAL

COMMENT

JOURNAL REFERENCE AUTHORS

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DEFINITION
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                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                             Center clone name: Mail-568N1
Center clone name: Ratistics
Sequencing vector: M3; L08821
Chemistry: Dye-primer Bodipp: 11% of reads
Chemistry: Dye-terminator Big. Dye: 89% of reads
Chemistry: Dye-terminator Big. Dye: 89% of reads
Chemistry: Dye-terminator Big. Dye: 89% of reads
Consensus quality: 168848 bases at least Q30
Consensus quality: 16863 bases at least Q30
Consensus quality: 180664 bases at least Q30
Estimated insert size: 180247; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   * NOTE: Estimated insert size may differ from sequence length

* NOTE: This is a "working draft' sequence. It currently

* NOTE: This is a "working draft' sequence. It currently

* consists of 18 contigs. The true order of the pieces

* is not known and thair order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N. but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                       Submitter (13-MAY-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Aug 13, 2000 Lhis sequence version replaced gi:9690226.
Tabor, P., Taylor, T., Vasquez, L., Vinson, R., Vo, O., Wahbah, M., Watlington, S., Weinstock, G., Weinstock, I.R., Williamson, A., Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig of 18030 bp in length
gap of unknown length
contig of 15422 bp in length
gap of unknown length
contig of 16547 bp in length
gap of unknown length
contig of 16547 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42030: contig of 42030 bp in length
42130: gap of unknown length
73896: contig of 31766 bp in length
73996: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10143 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 2782 bp in length
gap of unknown length
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of 9741 bp in length
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Center code: BCM
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                                                                            Direct Submission
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                                                                                                                                         Worley, K.C.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mumania; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 86524)

Muzny, D.M., Adams, C., Bailey, M., Barbaria, J., Blankenburg, K.,

Buodota, B., Bouck, J., Carter, M., Chen, Z., Coc, C.,

Burkett, C., Burrows, J., Carter, M., Chen, Z., Coc, C.,

Burkett, C., Durbin, K.J., Fernandez, C., Ferraguto, D.,

Dugan-Rocha, S., Durbin, K.J., Fernandez, C., Ferraguto, D.,

Forcum-Tansey, J., Frantaz, P., Hodgson, A., Hogues, M.,

Glevara, W., Harris, K., Hernandez, J., Hodgson, A., Hogues, M.,

Holloway, C., Bosak, H., Jackson, L.E., Jackson, L., Jack, Jackson, L., Jackson, L., Lichtarge, O., Liu, J., Liu, M., Logan, O., Lozado, R.J., Lu, J.,

Lucier, R., Martin, R., Martinez, C., McLeed, M.P., Mei, G., Morgan, M.,

Marris, S., Nash, S., Nelson, A., Nouyen, R., Nguyen, N., Nguyen, S.,

Ouiles, M., Reiter, D., Rives, M., Samuel, S., Say, J., Scherer, S.,

Shah, E., Shen, H., Simon, M., Samuel, S., Say, J., Scherer, S.,

Matlington, S., Weinstock, G., Weinstock, I.R., Williamson, A.,

Worley, K., Wren, J., Wrensford, G., Yu, W., Zhou, X., Nelson, D., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (23-NOV-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome 10 clone RP11-110, *** SEQUENCING IN PROGRESS ***, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1749 others
184776: contig of 1373 bp in length
184876: gap of unknown length
186142: contig of 1266 bp in length
186242: gap of unknown length
187419: contig of 1177 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: AC069255 from: 1 to: 187419
                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 12
Gaps: 0
Percent Identity: 83.333
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                                                                                                                                Location/Qualifiers
1. 187419
/organism="Homo sapiens"
                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                       /clone="RP11-568N1"
                                                                                                                                                                                                                                                 /chromosome="3"
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AC016140.10 GI:9966744
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LOCUS AC016140 86524 bp
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Unpublished
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                4.455
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                                                        184877
186143
186243
        183404
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Quality:
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Sequencing vector: M13: L08821
Session of the propriation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently
consists of 8 contigs. The true order of the pieces
is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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gap of unknown length
contig of 6057 bp in length
gap of unknown length
contig of 6720 bp in length
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17660: gap of unknown length
37082: contig of 19422 bp in length
37182: gap of unknown length
53268: contig of 16086 bp in length
53368: gap of unknown length
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gap of unknown length
contig of 5008 bp in length
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Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences. Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and CDNA sequences. Genes demonstrate at least two exons

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

ANNOTATION OF FEATURES:

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Worley, K.C.

Submitted (12-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Sequencing Sequencing Center, Department of Molecular and Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Jul SM, 2000 this sequence version replaced 91:9438826.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (16-AGC-1999) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (28-JUL-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 172581)
                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               AC009319.19 GI:9558561
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Direct Submission
                                                                Homo sapiens
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AC009319
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                                              SOURCE
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flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
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SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

338. .6929 / /note="Unigene cluster similar to: SEG_HSLPP Human lipoma /rpt.family="(CA)n" 15652. .15996 /note="Region similar to: Hs#S1813459 UI-HF-BNO-alf-f-08-0-UI.rl Homo sapiens CDNA: AW503943" complement(16516. .17018) /note="Region Similar to: Hs#S1739629 UI-H-BW0-ajp-d-04-0-UI.sl Homo sapiens cDNA: AW298030" 17132. .17835 /note="Region similar to: Hs#S2010443 EST387857 Homo sapiens cDNA: AW975748" /rpt_family="Alusc" complement(13047. .13192) /rpt_family="MIR" complement(13910. .14180) //note="Region similar to: Hs#S1034663 oml0h11.s1 Homo saplens CDNA: AA907068" /rpt_family="AT_rich" complement(9379. .9831) /note="Region similar to: Hs#S1816152 hd44d11.x1 Homo sapiens CDNA: AW511222" preferred partner (LPP) gene" 6449. .6622 9770. .10043 /rpt_family="Alux" complement(11625. .11879) /rpt_family="Alux" 12336. .12639 complement(14381 .14842) /rpt_family="LIPA3" 14843 .15191 /rpt_family="A-rich"
8121. .8205
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complement(8904. .9214)
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Length: 14
Gaps: 0
Percent Identity: 57.143
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complement(19962, .20058)
/rpt_family="L2"
complement(121429, .21723)
/rpt_family="AluSq"
21804, .21912
/rpt_family="LIM4"
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25419. .2570F
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25982. .2625
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28306. .28947
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31990. 3201
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/rpt_family="Alusq"
32348. .32360
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complement(33728. .34028)
/rpt_family="AluSg"
34159. .34213
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24039. 24058
rpt_family="AT_rich"
24159. 24458
/rpt_family="AluSq"
24458. 24658
/rpt_family="Li"
complement(25074. 2537
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31541. .31633
/rpt_family="LIMA7"
complement(31734. .319
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23175. .23407
/rpt_family="AluSq"
23446. .23726
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21990. .22716
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23767. .23831
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22720. .22894
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